

2314-227  
JLI:ch

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

10862 U.S. PTO  
09/749637  
12/28/00

In re patent application of: )  
Baldomero M. OLIVERA )  
Serial No.: (to be assigned) )  
Filed: 28 December 2000 )  
For: O-SUPERFAMILY CONOTOXIN )  
PEPTIDES )

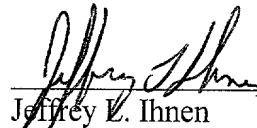
STATEMENT PURSUANT TO 37 CFR 1.821(f)

Assistant Commissioner for Patents  
Washington, D.C. 20231

Sir:

In the matter of the above-identified application, which is filed concurrently herewith, Applicants submit a computer diskette containing the Sequence Listing of the instant application. It is hereby certified that the paper and computer copies of these sequences are identical.

Respectfully submitted,



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<110> University of Utah Research Foundation
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McIntosh, J. Michael
Layner, Richard T.
Jones, Robert M.
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<151> 2000-10-27

<151> 2000-07-20

<151> 2000-06-26

<151> 1999-12-30

<160> 409

<170> PatentIn version 3.0

<210> 1

<211> 261

<212> DNA

<213> Conus gloriamaris

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<221> CDS

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tgg aca ttc gtc acg gct gat gac tcc gga aat gga atg gag att ctt 96  
Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Ile Leu  
20 25 30

ttt ccg aag gcg ggt cac gaa atg gag aac ctc gaa gtc tct aat cgg 144  
Phe Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Val Ser Asn Arg  
35 40 45

gtc aag ccg tgc cgt aaa gaa ggt caa ctt tgt gat ccg ata ttt caa 192  
Val Lys Pro Cys Arg Lys Glu Gly Gln Leu Cys Asp Pro Ile Phe Gln  
50 55 60

aac tgc tgc cgt ggc tgg aat tgc gtt ott ttc tgc gtc tgaaactacc 241  
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gtgatgtctt ctctccctc 261

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 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Ile Leu  
 20 25 30

Phe Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Val Ser Asn Arg  
 35 40 45

Val Lys Pro Cys Arg Lys Glu Gly Gln Leu Cys Asp Pro Ile Phe Gln  
 50 55 60

Asn Cys Cys Arg Gly Trp Asn Cys Val Leu Phe Cys Val  
 65 70 75

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<220>  
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<400> 4

003221 2236460



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 <213> Conus omaria

<400> 7

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 <212> PRT  
 <213> Conus omaria

<220>  
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 <212> DNA  
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<220>  
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gct gtg ctg ttc ttg acc gcc tgg aca ttc gtc acg gct gat gac tcc 99  
 Ala Val Leu Phe Leu Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser  
 10 15 20 25

aga aat gga atg gag aat ctt ttt ccg aag gca ggt cac gaa atg gag 147  
 Arg Asn Gly Met Glu Asn Leu Phe Pro Lys Ala Gly His Glu Met Glu  
 30 35 40

aac ctc gaa gac tct aaa cac agg cac cag gag aga ccg gac acc ggc 195  
 Asn Leu Glu Asp Ser Lys His Arg His Gln Glu Arg Pro Asp Thr Gly  
 45 50 55

gac aaa gaa gag atg ctg cta cag aga cag gtc aag ccg tgt cgt aaa 243

003221" 4E964259

Asp Lys Glu Glu Met Leu Leu Gln Arg Gln Val Lys Pro Cys Arg Lys  
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gaa cat caa ctt tgt gat ctg att ttt caa aac tgc tgc cgt ggc tgg 291  
Glu His Gln Leu Cys Asp Leu Ile Phe Gln Asn Cys Cys Arg Gly Trp  
75 80 85  
tat tgc gtt gtt ctg tct tgc act tgaaagctac ctgatgtgtt ctactcccat 345  
Tyr Cys Val Val Leu Ser Cys Thr  
90 95  
c 346

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<212> PRT  
<213> Conus textile

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20 25 30

Phe Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Asp Ser Lys His  
35 40 45

Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu  
50 55 60

Gln Arg Gln Val Lys Pro Cys Arg Lys Glu His Gln Leu Cys Asp Leu  
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Thr

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<213> Conus textile

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<223> Xaa at residue 1 may be Gln or pyro-Glu; Xaa at residue 4 may be  
Pro or hydroxy-Pro; Xaa at residue 23 may be Trp or bromo-Trp; Xa  
a at residue 24 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr  
, C-sulpho-Tyr or O-phospho-Tyr

<400> 11

008222" 1296460

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65

70

75

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 <213> Conus omaria

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 <222> (1)..(27)  
 <223> Xaa at residues 3 and 7 may be Pro or hydroxy-Pro; Xaa at residue 5 may be Glu or gamma-carboxy-Glu; Xaa at residue 10 may be Trp or bromo-Trp; Xaa at residue 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 14

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 1 5 10 15

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 <212> DNA  
 <213> Conus dalli

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 1 5 10 15  
 tgg aca ttc gtc acg gct gat gac tcc gga aat gga atg gag aat ctt 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu  
 20 25 30  
 ttt ccg aag gca cgt cac gaa atg gag aac ctc gaa gac tct aaa cac 144  
 Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His  
 35 40 45  
 agg cac cag gag aga ccg gac acg ggc gac aaa gaa gag atg ctg cta 192  
 Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu  
 50 55 60  
 cag aga cag gtc aag ccg tgt cgt aaa gaa cat caa ctt tgt gat ctg 240  
 Gln Arg Gln Val Lys Pro Cys Arg Lys Glu His Gln Leu Cys Asp Leu  
 65 70 75 80  
 att ttt caa aac tgc tgc cgt ggc tgg tat tgc ttg ctt cgt cct tgc 288  
 Ile Phe Gln Asn Cys Cys Arg Gly Trp Tyr Cys Leu Leu Arg Pro Cys  
 85 90 95  
 atc tgaaactacc gtgatgtctt ctctcccatc 321  
 Ile

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<400> 16

Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu  
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Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu  
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Ile Phe Gln Asn Cys Cys Arg Gly Trp Tyr Cys Leu Leu Arg Pro Cys  
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<210> 17
<211> 31
<212> PRT
<213> Conus dalli
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<220>
<221> SITE
<222> {1}..{31}
<223> Xaa at residue 24 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

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Gln Asn Cys Cys Arg Gly Xaa Xaa Cys Leu Leu Arg Xaa Cys Ile  
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 <213> Conus dalli

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 tgg aca ttc gtc acg gct gat gac tcc gga aat gga atg gag aat ctt 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu  
 20 25 30  
 ttt ccg aag gca cgt cac gaa atg gag aac ctc gaa gac tct aaa cac 144  
 Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His  
 35 40 45  
 agg cac cag gag aga ccg gac acg ggc gac aaa gaa gag atg ctg cta 192  
 Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu  
 50 55 60  
 cag aga cgg gtc aag ccg tgc agt gaa gaa ggt caa ctt tgt gat cca 240  
 Gln Arg Arg Val Lys Pro Cys Ser Glu Glu Gly Gln Leu Cys Asp Pro  
 65 70 75 80  
 ctt tct caa aac tgc tgc cgt ggc tgg cat tgc gtt ctt gtc tct tgc 288  
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 85 90 95  
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 Val

<210> 19  
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 <212> PRT  
 <213> Conus dalli

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 20 25 30  
 Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His  
 35 40 45  
 Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu  
 50 55 60  
 Gln Arg Arg Val Lys Pro Cys Ser Glu Glu Gly Gln Leu Cys Asp Pro  
 65 70 75 80

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Leu Ser Gln Asn Cys Cys Arg Gly Trp His Cys Val Leu Val Ser Cys  
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Val

<210> 20  
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<220>  
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Asn Cys Cys Arg Gly Xaa His Cys Val Leu Val Ser Cys Val  
                   20                  25                  30

<210> 21  
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 <213> Conus textile

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ttc ttg acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga 97  
 Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly  
                   15                  20                  25

ttg ggg aat ctt ttt tgg aat gca cat cac gaa atg aag aac ccc gaa 145  
 Leu Gly Asn Leu Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu  
                   30                  35                  40

gcc tct aaa ttg aac aag agg tgg tgc aaa caa agc ggt gaa atg tgt 193  
 Ala Ser Lys Leu Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys  
                   45                  50                  55                  60

aat ttg tta gac caa aac tgc tgc gac ggc tat tgc ata gta ctt gtc 241  
 Asn Leu Leu Asp Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val  
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tgc aca taaaactgcc gtgatgtctt ctct ccct ctgtgctacc tggcttgatc 297  
 Cys Thr

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tttgattggc gcggtgctgtt cactgggttat gaaccccccc cccccccccc ccccccccct 357

tccggctctc tggaggcctc ggggggttcaa catccaaata aagtgacag 406

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<211> 78  
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<400> 22

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Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu  
20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp  
50 55 60

Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr  
65 70 75

<210> 23  
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<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be  
Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Ty  
r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 23

Xaa Cys Lys Gln Asp Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys  
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Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr  
20 25

<210> 24  
<211> 27  
<212> PRT  
<213> Conus textile

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<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be  
Glu or gamma-carboxy-Glu; Xaa at residue 9 is Nle; Xaa at residue  
20 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-T

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yr or O-phospho-Tyr

<400> 24

Xaa Cys Lys Gln Asp Gly Xaa Xaa Cys Asn Leu Leu Asp Gln Asn Cys  
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Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr  
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1 5 10 15

tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ctt 96  
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu  
20 25 30

ttt tgc aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

aac aag agg tgg tgc aaa caa agc ggt gaa atg tgt aat ttg tta gac 192  
Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp  
50 55 60

caa aac tgc tgc gac ggc tat tgc ata gta ctt gtc tgc aca 234  
Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr  
65 70 75

taaaactgcc gtgatgtctt ctctccct c 265

<210> 26

<211> 78

<212> PRT

<213> Conus magus

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20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp

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tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ctt 96

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Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu  
 20 25 30

ttt tgc aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
 Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

aac aag agg tgg tgc aaa caa agc ggt gaa atg tgt aat ttg tta gac 192  
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 50 55 60

caa aac tgc tgc gac ggc tat tgc ata gta ctt gtc tgc aca 234  
 Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr  
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Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu  
 20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp  
 50 55 60

Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr  
 65 70 75

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 Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Ty  
 r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 31

Xaa Cys Lys Gln Ser Gly Xaa Met Cy. Asn Leu Leu Asp Gln Asn Cys  
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Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr

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25

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$\langle 211 \rangle$	27



<212> PRT  
<213> Conus ammiralis

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<400> 34

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Cys Xaa Gly Xaa Cys Ile Val Leu Val Cys Thr  
20 25

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<211> 256  
<212> DNA  
<213> Conus dalli

<220>  
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1 5 10 15  
  
tgg aca ttc gcc acg gct gat gac ccc aga aat gga ttg gag aat ctt 96  
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu  
20 25 30  
  
ttt ttg aag gca cat cac gaa atg aac ccc gaa gcc tct aag ttg aat 144  
Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser Lys Leu Asn  
35 40 45  
  
gag agg tgc ctt ggt ggt ggt gaa gtt tgt gat atc ttt ttt cca caa 192  
Glu Arg Cys Leu Gly Gly Gly Glu Val Cys Asp Ile Phe Phe Pro Gln  
50 55 60  
  
tgc tgt ggc tat tgc att ctt ctt ttc tgc aca taaaactacc gtgatgtcctt 245  
Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Thr  
65 70 75  
  
ctcctccct c 256

<210> 36  
<211> 75  
<212> PRT  
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<400> 36

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1 5 10 15

0974963 12200

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu  
20 25 30

Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser Lys Leu Asn  
35 40 45

Glu Arg Cys Leu Gly Gly Gly Glu Val Cys Asp Ile Phe Phe Pro Gln  
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Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Thr  
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<210> 37  
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<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue  
13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr, 125-I-  
Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 37

Cys Leu Gly Gly Gly Xaa Val Cys Asp Ile Phe Phe Xaa Gln Cys Cys  
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Gly Xaa Cys Ile Leu Leu Phe Cys Thr  
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<210> 38  
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Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu  
1 5 10

acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg 159  
Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly  
15 20 25 30

aat att ttt tcg aat gca cat cac gaa atg aag aat ccc gaa gcc tct 207  
Asn Ile Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser  
35 40 45

aaa ttg aac aag agg tgc cgt cta ggg gct gaa agt tgt gat gta att 255  
Lys Leu Asn Lys Arg Cys Arg Leu Gly Ala Glu Ser Cys Asp Val Ile  
50 55 60

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tca caa aac tgc tgc caa ggc acg tgc gtt ttt ttc tgc tta cca 300  
 Ser Gln Asn Cys Cys Gln Gly Thr Cys Val Phe Phe Cys Leu Pro  
           65                              70                              75

tgatgtcttc tattctcctc tgtgctacct ggttgatct ttcattagcg cgtgcctttc 360

actggttatg aacccccctga tccgactctc tggcagcctc gggggttcaa catccaaata 420

aaacgacagc acaatgacaa a 441

<210> 39

<211> 77

<212> PRT

<213> Conus gloriamaris

<400> 39

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1                              5                              10                              15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Ile  
           20                              25                              30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
           35                              40                              45

Asn Lys Arg Cys Arg Leu Gly Ala Glu Ser Cys Asp Val Ile Ser Gln  
           50                              55                              60

Asn Cys Cys Gln Gly Thr Cys Val Phe Phe Cys Leu Pro  
 65                              70                              75

<210> 40

<211> 26

<212> PRT

<213> Conus gloriamaris

<220>

<221> SITE

<222> (1)..(26)

<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue  
 26 may be Pro or hydroxy-Pro

<400> 40

Cys Arg Leu Gly Ala Xaa Ser Cys Asp Val Ile Ser Gln Asn Cys Cys  
 1                              5                              10                              15

Gln Gly Thr Cys Val Phe Phe Cys Leu Xaa  
           20                              25

<210> 41

<211> 446

<212> DNA

<213> Conus gloriamaris

00949637-123000

<222> (74) .. (304)

ggatccttgc acggtgaatt tggcttcaca gttttccact gtcgtctttc gcatcatcca 60

aaacatcacc aag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg 109  
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu  
1 5 10

ttc ttg acc gcc tgg aca ttc gcc acg gct gat gac ccc aga aat gga 157  
Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly  
15 20 25

ttg gag aaa ctt ttt tcg aat aca cat cac gaa atg aag aac ccc gaa 205  
Leu Glu Lys Leu Phe Ser Asn Thr His His Glu Met Lys Asn Pro Glu  
30 35 40

gcc tct aaa ttg aac aag agg tgc aaa caa gct gat gaa tct tgt aat 253  
Ala Ser Lys Leu Asn Lys Arg Cys Lys Gln Ala Asp Glu Ser Cys Asn  
45 50 55 60

gta ttt tca ctt gac tgc tgc acc ggc tta tgc ttg gga ttc tgc gta 301  
Val Phe Ser Leu Asp Cys Cys Thr Gly Leu Cys Leu Gly Phe Cys Val  
65 70 75

tgg tgatgtcttc tactcccoctc tgtgctacct ggcttgatct ttgattggcg 354  
Ser

tgtgcctttc attggttatg aacccccctg atccgattct ttggcggcct cggggggttca 414

acatccaaat aaagcgacag cacaataaaa aa 446

<213> Conus gloriamaris

<400> 42

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Lys Leu  
20 25 30

Phe Ser Asn Thr His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

Asn Lys Arg Cys Lys Gln Ala Asp Glu Ser Cys Asn Val Phe Ser Leu  
50 55 60

Asp Cys Cys Thr Gly Leu Cys Leu Gly Phe Cys Val Ser  
65 70 75

<210> 43

Trp Thr Phe Ala Thr Ala Ile Thr Arg Asn Gly Leu Gly Asn Leu Phe  
20 25 30

Pro Lys Asn His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu Asn  
 35 40 45

Lys Arg Cys Val Pro Tyr Glu Gly Pro Cys Asn Trp Leu Thr Gln Asn  
 50 55 60

Cys Cys Asp Glu Leu Cys Val Phe Phe Cys Leu  
 65 70 75

<210> 46  
 <211> 25  
 <212> PRT  
 <213> Conus gloriamaris

<220>  
 <221> SITE  
 <222> (1)..(25)  
 <223> Xaa at residue 2 and 7 may be Pro or hydroxy-Pro; Xaa at residue  
 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
 or O-phospho-Tyr; Xaa at residue 5 and 18 may be Glu or gamma-ca  
 rboxy-Glu ; Xaa at residue 10 may be Trp or bromo-Trp

<400> 46

Cys Val Xaa Xaa Xaa Gly Xaa Cys Asn Xaa Leu Thr Gln Asn Cys Cys  
 1 5 10 15

Asp Xaa Leu Cys Val Phe Phe Cys Leu  
 20 25

<210> 47  
 <211> 250  
 <212> DNA  
 <213> Conus magus

<220>  
 <221> CDS  
 <222> (1)..(231)

<400> 47  
 atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctc ttc ttg acc gtc 48  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Val  
 1 5 10 15  
 tgg aca ttc gcc acg gct gat gac tcc gga aat gga ttg gag aaa ctt 96  
 Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Lys Leu  
 20 25 30  
 ttt tcg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
 Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45  
 aac aag agg tgc aaa caa gct gat gaa cct tgt gat gta ttt tca ctt 192  
 Asn Lys Arg Cys Lys Gln Ala Asp Glu Pro Cys Asp Val Phe Ser Leu  
 50 55 60  
 gaa tgc tgc acc ggc ata tgt ctt gga ttc tgc acg tgg tgatgtcttc 241  
 Glu Cys Cys Thr Gly Ile Cys Leu Gly Phe Cys Thr Trp  
 65 70 75

002227" 46964250

250

<400> 48

Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Lys Leu  
20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

Asn Lys Arg Cys Lys Gln Ala Asp Glu Pro Cys Asp Val Phe Ser Leu  
50 55 60

Glu Cys Cys Thr Gly Ile Cys Leu Gly Phe Cys Thr Trp  
65 70 75

<210>	49
<211>	26
<212>	PRT
<213>	Conus magus

```
<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residue 6 and 14 may be Glu or gamma-carboxy-Glu; Xaa at r
      esidue 7 may be Pro or hydroxy-Pro; Xaa at residue 26may be Trp o
      r bromo-Trp
```

<400> 49

Cys Lys Gln Ala Asp Xaa Xaa Cys Asp Val Phe Ser Leu Xaa Cys Cys  
1 5 10 15

Thr Gly Ile Cys Leu Gly Phe Cys Thr Xaa  
20 25

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<210> 50
<211> 434
<212> DNA
<213> Conus textile
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<220>
<221> CDS
<222> (71)..(295)
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<400> 50
gccttgcacg gtgaatttgg cttcatagtt ttccactgtc gtctttggca tcatccaaaa 60
catcaccaag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc 109
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```

<220>
<221> SITE
<222> (1)..(25)
<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr, 125-
I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr.

```



&lt;400&gt; 52

Cys Leu Asp Ala Gly Xaa Val Cys Asp Ile Phe Phe Xaa Thr Cys Cys  
 1 5 10 15

Gly Xaa Cys Ile Leu Leu Phe Cys Ala  
 20 25

<210> 53  
 <211> 26  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> SITE  
 <222> (1)..(26)  
 <223> Xaa at residues 3 and 9 may be Glu or gamma-carboxy-Glu; Xaa at residue 7 may be Pro or hydroxy-Pro

&lt;400&gt; 53

Cys Ile Xaa Gln Phe Asp Xaa Cys Xaa Met Ile Arg His Thr Cys Cys  
 1 5 10 15

Val Gly Val Cys Phe Leu Met Ala Cys Ile  
 20 25

<210> 54  
 <211> 26  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> SITE  
 <222> (1)..(26)  
 <223> Xaa at residues 3, 7 and 13 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

&lt;400&gt; 54

Cys Ala Xaa Phe Leu His Xaa Cys Thr Phe Phe Phe Xaa Asn Cys Cys  
 1 5 10 15

Asn Ser Xaa Cys Val Gln Phe Ile Cys Leu  
 20 25

<210> 55  
 <211> 260  
 <212> DNA  
 <213> Conus omaria

<220>  
 <221> CDS  
 <222> (1)..(240)

&lt;400&gt; 55

atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc  
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

48

008222" 4E96460

Cys Leu Ala Xaa His Xaa Thr Cys Asn Ile Phe Thr Gln Asn Cys Cys  
1 5 10 15

<210> 60

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<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residues 3, 7 and 10 may be Pro or hydroxy-Pro.
```

Cys Ile Xaa His Phe Asp Xaa Cys Asp Xaa Ile Arg His Thr Cys Cys  
1 5 10 15  
Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile  
20 25

```
<220>
<221> CDS
<222> (1)..(228)
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```
<210> 62
<211> 76
<212> PRT
<213> Conus omaria
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Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Lys Asn Leu  
20 25 30



tgatgtcttc tctctaccc tc

262

<210> 65  
 <211> 80  
 <212> PRT  
 <213> Conus aulicus

<400> 65

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu  
 20 25 30

Phe Ser Lys Thr Gln His Lys Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

Asn Lys Arg Cys Lys Ala Glu Asn Glu Leu Cys Asn Ile Phe Ile Gln  
 50 55 60

Asn Cys Cys Asp Gly Thr Cys Leu Leu Ile Cys Ile Gln Asn Pro Gln  
 65 70 75 80

<210> 66  
 <211> 29  
 <212> PRT  
 <213> Conus aulicus

<220>  
 <221> SITE  
 <222> (1)..(29)  
 <223> Xaa at residues 4 and 6 may be Glu or gamma-carboxy-Glu; Xaa at residue 28 may be Pro or hydroxy-Pro

<400> 66

Cys Lys Ala Xaa Asn Xaa Leu Cys Asn Ile Phe Ile Gln Asn Cys Cys  
 1 5 10 15

Asp Gly Thr Cys Leu Leu Ile Cys Ile Gln Asn Xaa Gln  
 20 25

<210> 67  
 <211> 258  
 <212> DNA  
 <213> Conus aulicus

<220>  
 <221> CDS  
 <222> (1)..(228)

<400> 67

atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc gcc  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

48

09749637 "122300

tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg gat aat cgt 96  
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Asp Asn Arg  
           20                          25                          30

ttt tcg aag gca cgt cac gaa atg aat aac cgc aga gcc tct aaa ttg 144  
 Phe Ser Lys Ala Arg His Glu Met Asn Asn Arg Arg Ala Ser Lys Leu  
           35                          40                          45

aac aag agg tgc ctt gag ttt ggt gaa ctt tgt aat ttt ttt ttc cca 192  
 Asn Lys Arg Cys Leu Glu Phe Gly Glu Leu Cys Asn Phe Phe Phe Pro  
           50                          55                          60

acc tgc tgc ggc tat tgc gtt ctt ctt gtc tgc cta taaactaccg 238  
 Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu  
           65                          70                          75

tgatgtcttc tcttcccctc 258

<210> 68  
 <211> 76  
 <212> PRT  
 <213> Conus aulicus

<400> 68

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1                          5                          10                          15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Asp Asn Arg  
           20                          25                          30

Phe Ser Lys Ala Arg His Glu Met Asn Asn Arg Arg Ala Ser Lys Leu  
           35                          40                          45

Asn Lys Arg Cys Leu Glu Phe Gly Glu Leu Cys Asn Phe Phe Phe Pro  
           50                          55                          60

Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu  
 65                          70                          75

<210> 69  
 <211> 25  
 <212> PRT  
 <213> Conus aulicus

<220>  
 <221> SITE  
 <222> (1)..(25)  
 <223> Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at r  
       esidue 13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr  
       , 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phosph  
       o-Tyr

<400> 69

Cys Leu Xaa Phe Gly Xaa Leu Cys Asn Phe Phe Phe Xaa Thr Cys Cys

00822T 12800 094963 12800

1	5	10	15
Gly Xaa Cys Val Leu Leu Val Cys Leu			
	20	25	
<210> 70			
<211> 263			
<212> DNA			
<213> Conus dalli			
<220>			
<221> CDS			
<222> (1)..(231)			
<400> 70			
atg aaa ctg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg acc gcc			48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala			
1 5 10 15			
tgg aca ttt gtc atg gct gat gac tcc gga aat gga ttg gaa aat ctg			96
Trp Thr Phe Val Met Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu			
20 25 30			
ttt tgc aag gca cat cac gaa atg aag aac cct gaa gcc tct aaa ttg			144
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu			
35 40 45			
aac aag agg tgc gct caa agc agt gaa tta tgt gat gcg ctg gac tca			192
Asn Lys Arg Cys Ala Gln Ser Ser Glu Leu Cys Asp Ala Leu Asp Ser			
50 55 60			
gac tgc tgc agt ggt gtt tgc atg gta ttt ttc tgc cta taaaactgcc			241
Asp Cys Cys Ser Gly Val Cys Met Val Phe Phe Cys Leu			
65 70 75			
gtgatgtctt ctctatcccc tc			
			263
<210> 71			
<211> 77			
<212> PRT			
<213> Conus dalli			
<400> 71			
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala			
1 5 10 15			
Trp Thr Phe Val Met Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu			
20 25 30			
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu			
35 40 45			
Asn Lys Arg Cys Ala Gln Ser Ser Glu Leu Cys Asp Ala Leu Asp Ser			
50 55 60			
Asp Cys Cys Ser Gly Val Cys Met Val Phe Phe Cys Leu			
65 70 75			



<210> 72  
 <211> 26  
 <212> PRT  
 <213> Conus dalli

<220>  
 <221> SITE  
 <222> (1)..(26)  
 <223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu.

<400> 72

Cys Ala Gln Ser Ser Xaa Leu Cys Asp Ala Leu Asp Ser Asp Cys Cys  
 1 5 10 15

Ser Gly Val Cys Met Val Phe Phe Cys Leu  
 20 25

<210> 73  
 <211> 259  
 <212> DNA  
 <213> Conus distans

<220>  
 <221> CDS  
 <222> (1)..(228)

<400> 73  
 atg aaa ctg acg tgc gtg atg acc gtt gct gtg ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 tgg aca ttc gtc acg gct gaa gac ccc aga gat gga ttg agg aat ctt 96  
 Trp Thr Phe Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Arg Asn Leu  
 20 25 30  
 tta tcg aat gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
 Leu Ser Asn Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45  
 aac gag agg tgc ctt ggg ttt ggt gaa gct tgt ctt atg ctt tat tca 192  
 Asn Glu Arg Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu Tyr Ser  
 50 55 60  
 gac tgc tgc agc tat tgc gtt ggt gct gtc tgc cta taaaactacc 238  
 Asp Cys Cys Ser Tyr Cys Val Gly Ala Val Cys Leu  
 65 70 75  
 gtgatgtctt ctactcccat c 259

<210> 74  
 <211> 76  
 <212> PRT  
 <213> Conus distans

<400> 74

Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

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atg aaa ctg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ott 96  
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu  
20 25 30

ttt tcg aat gca cat cac gaa atg aag aac ccc gaa gct tct aaa ttg 144  
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

aac gag agg tgc ctt ggg ttt ggt gaa gtt tgc aat ttc ttt ttt cca 192  
Asn Glu Arg Cys Leu Gly Phe Gly Glu Val Cys Asn Phe Phe Phe Pro  
50 55 60

aac tgc tgc agc tat tgc gtt gct ctt gtc tgc cta taaaactacc 238  
Asn Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu  
65 70 75

gtgatgtctt ctattccct c 259

<210> 80  
<211> 76  
<212> PRT  
<213> Conus pennaceus

<400> 80

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu  
20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

Asn Glu Arg Cys Leu Gly Phe Gly Glu Val Cys Asn Phe Phe Phe Pro  
50 55 60

Asn Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu  
65 70 75

<210> 81  
<211> 25  
<212> PRT  
<213> Conus pennaceus

<220>  
<221> SITE  
<222> (1)..(25)  
<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue  
13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr, 125-I  
-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 81

Cys Leu Gly Phe Gly Xaa Val Cys Asn Phe Phe Phe Xaa Asn Cys Cys  
 1 5 10 15

Ser Xaa Cys Val Ala Leu Val Cys Leu  
 20 25

<210> 82  
 <211> 260  
 <212> DNA  
 <213> Conus pennaceus

<220>  
 <221> CDS  
 <222> (1)..(240)

<400> 82  
 atg aaa ctg acg tgc gtg atg ctc gtt gct gtg ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Val Met Leu Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 tgg aca ttc gcc acg gct gat gac tcc agc aat gga ctg gag aat ctt 96  
 Trp Thr Phe Ala Thr Ala Asp Asp Ser Ser Asn Gly Leu Glu Asn Leu  
 20 25 30  
 ttt tcg aag gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45  
 aac aag agg tgc att cca caa ttt gat cct tgt gac atg gta cgt cac 192  
 Asn Lys Arg Cys Ile Pro Gln Phe Asp Pro Cys Asp Met Val Arg His  
 50 55 60  
 act tgc tgc aaa ggg ttg tgc gta cta ata gcc tgc tct aaa act gcg 240  
 Thr Cys Cys Lys Gly Leu Cys Val Leu Ile Ala Cys Ser Lys Thr Ala  
 65 70 75 80  
 tgatgtcttc atctcccttc 260

<210> 83  
 <211> 80  
 <212> PRT  
 <213> Conus pennaceus

<400> 83  
 Met Lys Leu Thr Cys Val Met Leu Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Trp Thr Phe Ala Thr Ala Asp Asp Ser Ser Asn Gly Leu Glu Asn Leu  
 20 25 30  
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45  
 Asn Lys Arg Cys Ile Pro Gln Phe Asp Pro Cys Asp Met Val Arg His  
 50 55 60  
 Thr Cys Cys Lys Gly Leu Cys Val Leu Ile Ala Cys Ser Lys Thr Ala

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<210> 84
<211> 29
<212> PRT
<213> Conus pennaceus

<220>
<221> SITE
<222> (1)..(29)
<223> Xaa at residues 3 and 7 may be Pro or hydroxy-Pro.
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Cys Ile Xaa Gln Phe Asp Xaa Cys Asp Met Val Arg His Thr Cys Cys  
1 5 10 15

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<210> 85
<211> 260
<212> DNA
<213> Conus pennaceus
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```
<400> 85
atg aaa ctg acg tgc ttg atg atc gtt gct gtg ctg ttc ttg acc gcc      48
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1          5          10          15
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ttt tgc aag aca caa cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
Phe Ser Lys Thr Gln His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

aac tgc tgc gac ggc aag tgc ctt ttt ttc tgc ata caa att cca gag 240  
Asn Cys Cys Asp Gly Lys Cys Leu Phe Phe Cys Ile Gln Ile Pro Glu  
65 70 75 80

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<210> 86
<211> 80
<212> PRT
<213> Conus pennaceus
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Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

[illegible]

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<400> 91
ggtcgacatc atcatcatcg atccatctgt ccatccatcc attcattcat tcgctgccag      60
actgtcataa atattcgagt ctctccttct gtttgtatct gacaga ttg aac aag      115
                                   Leu Asn Lys
                                   1

```



agg tgc ctt gac ggt ggt gaa att tgt ggt att ttg ttt cca agc tgc 163  
 Arg Cys Leu Asp Gly Gly Glu Ile Cys Gly Ile Leu Phe Pro Ser Cys  
           5                          10                          15

tgc agt ggg tgg tgc att gtt ctc gtc tgc gca tgaaactacc gtgatgtctt 216  
 Cys Ser Gly Trp Cys Ile Val Leu Val Cys Ala  
           20                          25                          30

ctactcccct ctagtagtag taggcggccg ctctagagga tccaagctta cgtacgcgtg 276

catgcgacgt catagctctt ctatagtgtc acctaaattc aattcactgg ccgtcgtttt 336

acaacgtcgt gactgggaaa accctggcgt taccacaactt aatcgccttg cagcacatcc 396

ccctttcgcc agctggcgta atagcgaaga ggcccgacc gatcgccctt cccaacaagt 456

tgcgcagcct gaatggcgaa tgggacgcgc cctgtagcgg cgcattaagc gcggcgggtg 516

tgggtggttac gcgcaccgtg accgctacac ttgccagcgc cctagccgcc cgctcctttc 576

gctttcttcc ctctctttct cgcacgttcg gccggctttc cccgtcaagc tctaaatcgg 636

gggcttcctt tttt 650

<210> 92

<211> 30

<212> PRT

<213> Conus omaria

<400> 92

Leu Asn Lys Arg Cys Leu Asp Gly Gly Glu Ile Cys Gly Ile Leu Phe  
           1                          5                          10                          15

Pro Ser Cys Cys Ser Gly Trp Cys Ile Val Leu Val Cys Ala  
                           20                          25                          30

<210> 93

<211> 26

<212> PRT

<213> Conus omaria

<220>

<221> SITE

<222> (1)..(26)

<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue  
 13 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Trp or bro  
 mo-Trp

<400> 93

Cys Leu Asp Gly Gly Xaa Ile Cys Gly Ile Leu Phe Xaa Ser Cys Cys  
           1                          5                          10                          15

Ser Gly Xaa Cys Ile Val Leu Val Cys Ala  
                           20                          25

<210> 94

<211> 618

003221" 2E964260

<212> DNA  
<213> Conus marmoreus

<220>  
<221> CDS  
<222> (107)..(193)

<400> 94  
ggtcgacatc atcatcatcg atccatctgt ccattccatcc atccattcat tcgctgccag 60  
actgtaataa atattcgagt ctctctttct gtttgtatct gacaga ttg aac aag 115  
Leu Asn Lys  
1  
agg tgc ctt gag ttt ggt gaa gtt tgt aat ttt ttt ttc cca acc tgc 163  
Arg Cys Leu Glu Phe Gly Glu Val Cys Asn Phe Phe Phe Pro Thr Cys  
5 10 15  
tgc ggc tat tgc gtt ctt ctt gtc tgc cta taaaactacc gtgatgtctt 213  
Cys Gly Tyr Cys Val Leu Leu Val Cys Leu  
20 25  
ctactcccct ctagtagtag taggcggccg ctctagagga tccaagctta cgtacgcgtg 273  
catgcgacgt catagctctt ctatagtgtc acctaaattc aattcactgg ccgtcgtttt 333  
acaacgtcgt gactgggaaa accctggcgt taccacaactt aatcgccttg cagcacatcc 393  
ccctttcggc agctggcgta atagcgaaga ggccccgacc gatcgccctt cccaacagtt 453  
gcgagcgtg aatggcggaat gggacgcgcc ctgtagcggc gcattaagcg cggcgggtgt 513  
ggtggttacg cgcagcgtga ccgtacact tgcagcgccc tagcgccgc tcctttcgt 573  
ttcttccctt cctttctcgc cacgttcgcc ggctttcccc gtcaa 618

<210> 95  
<211> 29  
<212> PRT  
<213> Conus marmoreus

<400> 95  
Leu Asn Lys Arg Cys Leu Glu Phe Gly Glu Val Cys Asn Phe Phe Phe  
1 5 10 15  
Pro Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu  
20 25

<210> 96  
<211> 25  
<212> PRT  
<213> Conus marmoreus

<220>  
<221> SITE  
<222> (1)..(25)  
<223> Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at r  
esidue 13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr  
, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phosph  
o-Tyr

&lt;400&gt; 96

Cys Leu Xaa Phe Gly Xaa Val Cys Asn Phe Phe Phe Xaa Thr Cys Cys  
 1 5 10 15

Gly Xaa Cys Val Leu Leu Val Cys Leu  
 20 25

&lt;210&gt; 97

&lt;211&gt; 444

&lt;212&gt; DNA

&lt;213&gt; Conus marmoreus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (150)..(236)

&lt;400&gt; 97

gaaagctggg acgcctgcag gtaccgggtcc ggaattcccg ggctgcacatc atcatcatca 60

togatccatc tgtccatcca tccattcatt cattcgctgc cagaactgtaa taaatattcg 120

agttttctct tctgtttgta tctgacagg ttg aac aag agg tgc caa gag ttc 173  
 Leu Asn Lys Arg Cys Gln Glu Phe  
 1 5

ggg gaa gtt tgt aat ttt ttt ttc cca gac tgc tgc ggc tat tgc gtt 221  
 Gly Glu Val Cys Asn Phe Phe Phe Pro Asp Cys Cys Gly Tyr Cys Val  
 10 15 20

ctt tta ctc tgc ata taaaactacc gtgatgtctt ctcttcccat ctagtagtag 276  
 Leu Leu Leu Cys Ile  
 25

tagtagtagt aggcggccgc tctagaggat ccaagcttac gtacgcgtgc atgcgacgtc 336

atagctcttc tatagtgtca cctaaattca attcactggc cgtcgtttta caaccgtcgt 396

gactgggaaa accctggcgt tcccaactta attgccttg cagcacat 444

&lt;210&gt; 98

&lt;211&gt; 29

&lt;212&gt; PRT

&lt;213&gt; Conus marmoreus

&lt;400&gt; 98

Leu Asn Lys Arg Cys Gln Glu Phe Gly Glu Val Cys Asn Phe Phe Phe  
 1 5 10 15

Pro Asp Cys Cys Gly Tyr Cys Val Leu Leu Cys Ile  
 20 25

&lt;210&gt; 99

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Conus marmoreus

&lt;220&gt;

003327 4E964260

<400> 99

Gly Xaa Cys Val Leu Leu<sup>\*</sup> Leu Cys Ile  
20 25

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<220>
<221> CDS
<222> (153) .. (242)
```

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<400> 100
ttttgaagcn ggtacgcctg caggtagccg tccggaattc ccgggtcgac atcatcatca      60
tcatcgatcc atctgtccat ccattccatt attcattcgc taccagactg taataaatat      120
tcgggtctct ctttctgttt gtatctgaca ga ttg gac aag agg tgc att cca      173
                Leu Asp Lys Arg Cys Ile Pro
                1         5

```

cat ttt gac cct tgt gac ccg ata cgc cac acc tgc tgc ttt ggc ctg 221  
His Phe Asp Pro Cys Asp Pro Ile Arg His Thr Cys Cys Phe Gly Leu  
10 15 20

```
tgc cta cta ata gcc tgc atc taaaactgcc gtgatgtctt ctctccocct      272
Cys Leu Leu Ile Ala Cys Ile
      25                      30
```

ctagtagtag taggcggccg ctctagagga tccaagctta cgtacgcgtg catgcgacgt	332
catagctctt ctatagtgtc acctaaattc aattcaactgg ccgtcgtttt acaacgtcgt	392
gactgggaaa acctggcgt taccctaactt aatcgccttg cagcacatcc ccttttcgcc	452
agctggcgta atagcgaaga ggcccgacc gatcgcctt cccaacagtt gcgcagcctg	512
aatggcgaat gggaocgcc ctgtagcggc gct	545

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<210> 101
<211> 30
<212> PRT
<213> Conus omaria
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<400> 101

His Thr Cys Cys Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile  
20 25 30

```
<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residues 3, 7 and 10 may be Pro or hydroxy-Pro.
```

<400> 102

Cys Ile Xaa His Phe Asp Xaa Cys Asp Xaa Ile Arg His Thr Cys Cys  
1 5 10 15

Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile  
20 25

<210> 103  
<211> 534  
<212> DNA  
<213> *Conus omaria*

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<220>
<221> CDS
<222> (140)..(226)
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```

<400> 103
ggtagcgctg caggtaccgg tccggaattc ccgggtcgac atcatcatca tcgatccatc 60
tgtccatcca tccattcttt catttgctgc cagactgtaa taaatattcg agtctctctt 120
tctgtttgta tctgacaga ttg aac aag agg tgc ctt gag ttt ggt gaa gtt 172
                Leu Asn Lys Arg Cys Leu Glu Phe Gly Glu Val
                1          5          10
tgt aat ttt ttt ttc cca acc tgc tgc ggc tat tgc gtt ctt ctt gtc 220
Cys Asn Phe Phe Phe Pro Thr Cys Cys Gly Tyr Cys Val Leu Leu Val
          15          20          25
tgc cta taaaactacc gtgatgtctt ctcttccct ctagtagtag taggcggcgg 276
Cys Leu

ctctagagga tccaagctta cgtacgcgtg catgcgacgt catagctctt ctatagtgtc 336
acctaaattc aattcaactgg ccgtcgtttt acaacgtcgt gactgggaaa accctggcct 396

```

tacccaactt aatcgcccttg cagcacatcc ccctttcgcc agctggcgta atagcgaaga 456  
 ggcccgacc gatcgccctt cccaacagtt ggcagcctg aatggcgaat gggacgcgcc 516  
 ctgtagcggc gcattaag 534

<210> 104  
 <211> 29  
 <212> PRT  
 <213> Conus omaria

<400> 104

Leu Asn Lys Arg Cys Leu Glu Phe Gly Glu Val Cys Asn Phe Phe Phe  
 1 5 10 15

Pro Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu  
 20 25

<210> 105  
 <211> 25  
 <212> PRT  
 <213> Conus omaria

<220>  
 <221> SITE  
 <222> (1)..(25)  
 <223> Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at r  
 esidue13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr  
 , 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phosph  
 o-Tyr

<400> 105

Cys Leu Xaa Phe Gly Xaa Val Cys Asn Phe Phe Phe Xaa Thr Cys Cys  
 1 5 10 15

Gly Xaa Cys Val Leu Leu Val Cys Leu  
 20 25

<210> 106  
 <211> 200  
 <212> DNA  
 <213> Conus obscurus

<220>  
 <221> CDS  
 <222> (73)..(180)

<400> 106  
 cgatccatct gtccatccat ccattcgctt gtctgctgcc aaactgtaat aaataaccga 60

gtctctctgt tt gta tct gac aga tcg aaa aag caa tgc cgt caa aat ggt 111  
 Val Ser Asp Arg Ser Lys Lys Gln Cys Arg Gln Asn Gly  
 1 5 10

gaa gtg tgt gat gcg aat ttg gca cac tgc tgc agt ggc ccg tgt ttt 159  
 Glu Val Cys Asp Ala Asn Leu Ala His Cys Cys Ser Gly Pro Cys Phe  
 15 20 25

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200

<400> 107

Asp Ala Asn Leu Ala His Cys Cys Ser Gly Pro Cys Phe Leu Phe Cys  
20 25 30

<210>	108
<211>	32
<212>	PRT
<213>	Conus obscurus

```
<220>
<221> SITE
<222> (1)..(32)
<223> Xaa at residue 10 may be Glu or gamma-carboxy-Glu; Xaa at residue
s 23 and 32 may be Pro or hydroxy-Pro
```

<400> 108

Ala His Cys Cys Ser Gly Xaa Cys Phe Leu Phe Cys Leu Asn Gln Xaa  
20 25 30

```
<210> 109
<211> 262
<212> DNA
<213> Conus ammiralis
```

$\langle 220 \rangle$   
 $\langle 221 \rangle$  CDS  
 $\langle 222 \rangle$  (1) .. (231)

<400> 109

tgg	aca	ttt	gcc	acg	gct	gat	gac	tcc	gga	aat	gga	ttg	gaa	aat	ctt	96
Trp	Thr	Phe	Ala	Thr	Ala	Asp	Asp	Ser	Gly	Asn	Gly	Leu	Glu	Asn	Leu	
		20						25				30				

ttt tgc aag gca cat cac gaa atg aag aac ccc aaa gcc tct aaa ttg 144  
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Ala Ser Lys Leu

```
<210> 110
<211> 77
<212> PRT
<213> Conus ammiralis
```

Met Lys Leu Thr Cys Val Met Ile Ile Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu  
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Ala Ser Lys Leu  
35 40 45

Asn Lys Arg Cys Thr Gln Ser Gly Glu Leu Cys Asp Val Ile Asp Pro  
50 55 60

Asp Cys Cys Asn Asn Phe Cys Ile Ile Phe Phe Cys Ile  
65 70 75

```
<210> 111
<211> 26
<212> PRT
<213> Conus ammiralis
```

```
<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
13 may be Pro or hydroxy-Pro
```

 $\langle 400 \rangle$  111

Cys Thr Gln Ser Gly Xaa Leu Cys Asp Val Ile Asp Xaa Asp Cys Cys  
1 5 10 15

Asn Asn Phe Cys Ile Ile Phe Phe Cys Ile  
20 25

```
<210> 112
<211> 286
<212> DNA
<213> Conus textile
```



<400> 112

<220>

<221> SITE  
 <222> (1)..(26)  
 <223> Xaa at residues 3 and 13 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 114

Cys Ala Xaa Phe Leu His Leu Cys Thr Phe Phe Phe Xaa Asn Cys Cys  
 1 5 10 15

Asn Gly Xaa Cys Val Gln Phe Ile Cys Leu  
 20 25

<210> 115  
 <211> 484  
 <212> DNA  
 <213> Conus marmoreus

<220>  
 <221> CDS  
 <222> (74)..(304)

<400> 115  
 ggatcctagc acagtgaatt tggcttcaca gttttccact gtcgtctttg gcatcatcca 60  
 aaacatcacc aag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg 109  
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu  
 1 5 10  
 ttc ttg acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga 157  
 Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly  
 15 20 25  
 ttg gag aat ctt ttt tgc aag gca cat cac gaa atg aag aac ccc aaa 205  
 Leu Glu Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys  
 30 35 40  
 gac tct aaa ttg aac aag agg tgc ctt gac gct ggt gaa atg tgt gat 253  
 Asp Ser Lys Leu Asn Lys Arg Cys Leu Asp Ala Gly Glu Met Cys Asp  
 45 50 55 60  
 ctt ttt aat tca aaa tgc tgc agt ggg tgg tgc att att ctc ttc tgc 301  
 Leu Phe Asn Ser Lys Cys Cys Ser Gly Trp Cys Ile Ile Leu Phe Cys  
 65 70 75  
 gca taaaactacc gtgatgtctt ctactcccct ctgtgctacc tggcttgatc 354  
 Ala  
 tttgattggc gcgtgccctt cactgggttat gaacccccct gatccgactc tctggcgggc 414  
 tcggggggttc aacatccaaa taaagccgac acgatactga cgtagaaaaa aaaaaaaaaa 474  
 aaaaaaaaaa 484

<210> 116  
 <211> 77  
 <212> PRT  
 <213> Conus marmoreus  
 <400> 116

003221 48460

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu  
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Asp Ser Lys Leu  
35 40 45

Asn Lys Arg Cys Leu Asp Ala Gly Glu Met Cys Asp Leu Phe Asn Ser  
50 55 60

Lys Cys Cys Ser Gly Trp Cys Ile Ile Leu Phe Cys Ala  
65 70 75

<210> 117

<211> 26

<212> PRT

<213> Conus marmoreus

<220>

<221> SITE

<222> (1)..(26)

<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue  
19 may be Trp or bromo-Trp

<400> 117

Cys Leu Asp Ala Gly Xaa Met Cys Asp Leu Phe Asn Ser Lys Cys Cys  
1 5 10 15

Ser Gly Xaa Cys Ile Ile Leu Phe Cys Ala  
20 25

<210> 118

<211> 427

<212> DNA

<213> Conus marmoreus

<220>

<221> CDS

<222> (19)..(249)

<400> 118

gccgaaaaca tcaccaa<sup>g</sup> atg aaa ctg acg agc atg atg atc gtt gct gtg 51  
Met Lys Leu Thr Ser Met Met Ile Val Ala Val  
1 5 10

ctg ttc ttg acc gcc tgg aca ttc gtc acg gct gac gac tcc gga aat 99  
Leu Phe Leu Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn  
15 20 25

gga ttg gag aat ctt ttt tgc aag gca cat cac gag atg aag aac ccc 147  
Gly Leu Glu Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro  
30 35 40

aaa gac tct aaa ttg aac aag agg tgc ctt gac ggt ggt gaa att tgt 195

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Lys Asp Ser Lys Leu Asn Lys Arg Cys Leu Asp Gly Gly Glu Ile Cys  
 45 55

ggt att ttg ttt cca agc tgc tgc agt ggg tgg tgc att gtt ctc gtc 243  
 Gly Ile Leu Phe Pro Ser Cys Cys Ser Gly Trp Cys Ile Val Leu Val  
 60 65 70 75

tgc gca tgaaactacc gtgatgtctt ctactcccct ctgtgctacc tggcttgatc 299  
 Cys Ala

tttgattggc gcgtgccctt cactgggttat gaacccccct gatccgactc tctggcggcc 359

tcggggggttc aacatccaaa taaagcgaca cgacaatgac aaaaaaaaaa aaaaaaaaaa 419

aaaaaaaaa 427

<210> 119  
 <211> 77  
 <212> PRT  
 <213> Conus marmoreus

<400> 119

Met Lys Leu Thr Ser Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu  
 20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Asp Ser Lys Leu  
 35 40 45

Asn Lys Arg Cys Leu Asp Gly Gly Glu Ile Cys Gly Ile Leu Phe Pro  
 50 55 60

Ser Cys Cys Ser Gly Trp Cys Ile Val Leu Val Cys Ala  
 65 70 75

<210> 120  
 <211> 26  
 <212> PRT  
 <213> Conus marmoreus

<220>  
 <221> SITE  
 <222> (1)..(26)  
 <223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue  
 13 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Trp or bro  
 mo-Trp

<400> 120

Cys Leu Asp Gly Gly Xaa Ile Cys Gly Ile Leu Phe Xaa Ser Cys Cys  
 1 5 10 15

Ser Gly Xaa Cys Ile Val Leu Val Cys Ala

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25

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<220>
<221> CDS
<222> (70)..(303)
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```
<210> 122
<211> 78
<212> PRT
<213> Conus marmoreus
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Met Lys Leu Thr Cys Met Met Ile Glu Ala Glu Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu  
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln  
50 55 60

```
<210> 123
<211> 27
<212> PRT
<213> Conus marmoreus
```

```

<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residues 2 and 26 may be Pro or hydroxy-Pro; Xaa at residues 6 and 12 may be Glu or gamma-carboxy-Glu; Xaa at residues 17 and 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

```

<400> 123

Cys Xaa Asn Thr Gly Xaa Leu Cys Asp Val Val Xaa Gln Asn Cys Cys  
1 5 10 15

Xaa Thr Xaa Cys Phe Ile Val Val Cys Xaa Ile  
20 25

```
<210> 124
<211> 470
<212> DNA
<213> Conus marmoreus
```

```
<220>
<221> CDS
<222> (67) .. (312)
```

<400> 124  
ttgcacggtg aatttcgctt atatttttct actgtcgtct ttggcatcat ccaaaacatc 60

```

accaag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg      108
      Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu
      1              5              10

```

acc gcc tgg aca ttc gtc acg gct gtg cct cac tcc agc gat gta ttg 156  
Thr Ala Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val Leu  
15 20 25 30

gag aat ctt tat ctg aag gca ctt cac gaa acg gaa aac cac gaa gcc 204  
Glu Asn Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala  
35 40 45

tct aaa ttg aac gtg aga gac gac gag tgc gaa cct cct gga gat ttt 252  
Ser Lys Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe  
50 55 60

tgt ggc ttt ttt aaa att ggg ccg cct tgc tgc agt ggc tgg tgc ttc 300  
Cys Gly Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe  
65 70 75

ctc tgg tgc gcc taaaactgcc gtgatgtctt ctattcccct ctgtgctacc 352  
Leu Trp Cys Ala  
80

tggttgatc tttgattggc gcgtgccctt cagtggttat gaacccccct gatccgactc 412

tctggggggcc tcggggggttc aacatccaaa taaagctgac aacacaataa aaaaaaaaa

470

<210> 125  
 <211> 82  
 <212> PRT  
 <213> Conus marmoreus

<400> 125

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val Leu Glu Asn  
 20 25 30

Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys  
 35 40 45

Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly  
 50 55 60

Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp  
 65 70 75 80

Cys Ala

<210> 126  
 <211> 30  
 <212> PRT  
 <213> Conus marmoreus

<220>  
 <221> SITE  
 <222> (1)..(30)  
 <223> Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at r  
 esidues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residue  
 s 24 and 28 may be Trp or bromo-Trp

<400> 126

Asp Asp Xaa Cys Xaa Xaa Xaa Gly Asp Phe Cys Gly Phe Phe Lys Ile  
 1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Leu Xaa Cys Ala  
 20 25 30

<210> 127  
 <211> 277  
 <212> DNA  
 <213> Conus striatus

<220>  
 <221> CDS  
 <222> (1)..(246)

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<400> 127  
 atg aaa ctg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 tgg aca ttc gtc acg gct gtg cct cac tcc agc gat gca ttg gag aat 96  
 Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Ala Leu Glu Asn  
 20 25 30  
 ctt tat ctg aag gca ctt cac gaa acg gaa aac cac gaa gcc tct aaa 144  
 Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys  
 35 40 45  
 ttg aac gtg aga gac gac gag tgc gaa cct cct gga gat ttt tgt ggc 192  
 Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly  
 50 55 60  
 ttt ttt aaa att ggg ccg cct tgc tgc agt ggc tgg tgc ttc ctc tgg 240  
 Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp  
 65 70 75 80  
 tgc gca taaaactgcc gtgatgtctt ctctccct c 277  
 Cys Ala

<210> 128  
 <211> 82  
 <212> PRT  
 <213> Conus striatus

<400> 128

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Ala Leu Glu Asn  
 20 25 30  
 Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys  
 35 40 45  
 Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly  
 50 55 60  
 Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp  
 65 70 75 80  
 Cys Ala

<210> 129  
 <211> 30  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> SITE

009927 13200 7E964260



<223> Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at residues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residues 24 and 28 may be Trp or bromo-Trp

Asp Asp Xaa Cys Xaa Xaa Xaa Gly Asp Phe Cys Gly Phe Phe Lys Ile  
1 5 10 15

<213> Conus omaria

atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

tgg	aca	ttc	gtc	acg	gct	gtg	cct	cac	tcc	agc	aat	gca	ttg	gaa	aat		96
Trp	Thr	Phe	Val	Thr	Ala	Val	Pro	His	Ser	Ser	Asn	Ala	Leu	Glu	Asn		
		20					25					30					

ctt tat ctg aag gca cgt cac gaa atg gaa aac ccc gaa gcc tct aaa 144  
 Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys  
 35 40 45

ttg aac acg aga gac gac gat tgc gaa cct cct gga aat ttt tgt ggc 192  
 Leu Asn Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly  
 50 55 60

atg ata aaa att ggg cgg cct tgc tgc agt ggc tgg tgc ttt ttc gcc 240  
Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala  
65 70 75 80

tgc gcc taaaactgcc gtgatgtctt ctctcccoct c 277  
Cys Ala

<213> Conus omaria

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn  
20 25 30



Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala  
65 70 75 80

tgc gcc taaaactgcc gtgatgtctt ctctccct c  
Cys Ala

277

<210> 134  
<211> 82  
<212> PRT  
<213> Conus aulicus

<400> 134

Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn  
20 25 30

Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys  
35 40 45

Leu Asn Thr Arg Asp Tyr Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly  
50 55 60

Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala  
65 70 75 80

Cys Ala

<210> 135  
<211> 30  
<212> PRT  
<213> Conus aulicus

<220>  
<221> SITE  
<222> (1)..(30)  
<223> Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,  
O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 5 may be Glu or  
gamma-carboxy-Glu; Xaa at residues 6, 7, 18 and 19 may be Pro or  
hydroxy-Pro; Xaa at residue 24 may be Trp or bromo-Trp

<400> 135

Asp Xaa Asp Cys Xaa Xaa Xaa Gly Asn Phe Cys Gly Met Ile Lys Ile  
1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Ala Cys Ala  
20 25 30

<210> 136  
<211> 685  
<212> DNA

0082221" 2E96H460

<213> Conus marmoreus

<220>

<221> CDS

<222> (111)..(212)

<400> 136

ggtcgacatc atcatcatca tcgatccatc tgtccatcca tctattcatt cattcgtggc 60

caaaactgtaa taaataatgc aagtctctct ttctgtttgt atctgacaga ttg aac 116  
Leu Asn  
1

acg aga gac gac gat tgc gaa cct cct gga aat ttt tgt ggc atg ata 164  
Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly Met Ile  
5 10 15

aaa att ggg ccg cct tgc tgc agt ggc tgg tgc ttt ttc gcc tgc gcc 212  
Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala Cys Ala  
20 25 30

taaaactgcc gtgatgtctt ctcttccct ctagtagtag taggcggccg ctctagagga 272

tccaagctta cgtacgctg catgcgacgt catagctctt ctatagtgtc acctaaattc 332

aattcactgg ccgtcgtttt acaacgtcgt gactgggaaa accctggcgt taccctaactt 392

aatgccttg cagcacatcc ccctttcgcc agctggcgta atagcgaaga ggcccgacc 452

gatgcctt cccaacagtt ggcagcctg aatggcgaat gggacgcgcc ctgtagcggc 512

gcattaagcg cggcggtgt ggtggttac cgcagcgt gaccgcgtac acttgccagc 572

gocctagcgc ccgtccttt cgctttctt ctccctttct cgccacgttc gccggctttt 632

cccgtaagc tctaaatcg gggctcctt aggtccgat ttaagtgtt tac 685

<210> 137

<211> 34

<212> PRT

<213> Conus marmoreus

<400> 137

Leu Asn Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly  
1 5 10 15

Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala  
20 25 30

Cys Ala

<210> 138

<211> 30

<212> PRT

<213> Conus marmoreus

<220>

<221> SITE

008221" 4E954260

<222> (1)..(30)  
 <223> Xaa at residue 5 may be Glu or gamma-carboxy-Glu; Xaa at residues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residue 24 may be Trp or bromo-Trp

<400> 138

Asp Asp Asp Cys Xaa Xaa Xaa Gly Asn Phe Cys Gly Met Ile Lys Ile  
 1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Ala Cys Ala  
 20 25 30

<210> 139  
 <211> 126  
 <212> DNA  
 <213> Conus regius

<220>  
 <221> CDS  
 <222> (1)..(96)

<400> 139  
 ttg aac cag aga gac tgc ctt agt aaa aac gct ttc tgt gcc tgg ccg 48  
 Leu Asn Gln Arg Asp Cys Leu Ser Lys Asn Ala Phe Cys Ala Trp Pro  
 1 5 10 15

ata ctt gga cca ctg tgc tgc agt ggc tgg tgc tta tac gtc tgc atg 96  
 Ile Leu Gly Pro Leu Cys Cys Ser Gly Trp Cys Leu Tyr Val Cys Met  
 20 25 30

taaaactgcc gtgatgtctt ctatcccctc 126

<210> 140  
 <211> 32  
 <212> PRT  
 <213> Conus regius

<400> 140

Leu Asn Gln Arg Asp Cys Leu Ser Lys Asn Ala Phe Cys Ala Trp Pro  
 1 5 10 15

Ile Leu Gly Pro Leu Cys Cys Ser Gly Trp Cys Leu Tyr Val Cys Met  
 20 25 30

<210> 141  
 <211> 28  
 <212> PRT  
 <213> Conus regius

<220>  
 <221> SITE  
 <222> (1)..(28)  
 <223> Xaa at residues 11 and 22 may be Trp or bromo-Trp; Xaa at residues 12 and 16 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

003222T" / E96H/60

Gly Asp Asp Cys Leu Ala Val Lys Lys Asn Cys Gly Phe Xaa Lys Leu

<210>	148
<211>	345
<212>	DNA
<213>	Conus aurisiacus





<221> SITE  
 <222> (1)..(27)  
 <223> Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 25 may be Trp or bromo-Trp

<400> 150

Asp Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His Xaa Gly Leu  
 1 5 10 15

Cys Cys Ser Xaa Ile Cys Ile Val Xaa Cys Thr  
 20 25

<210> 151  
 <211> 412  
 <212> DNA  
 <213> Conus purpurascens

<220>  
 <221> CDS  
 <222> (1)..(243)

<400> 151  
 atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg act gcc 48  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 tgg aca ttc gtc acg gct gat gac tcc aaa aat gga ctg gag aat cat 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His  
 20 25 30  
 ttt tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg 144  
 Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu  
 35 40 45  
 gac aaa aag gaa gcc tgc tat gcg cct ggt act ttt tgt ggc ata aag 192  
 Asp Lys Lys Glu Ala Cys Tyr Ala Pro Gly Thr Phe Cys Gly Ile Lys  
 50 55 60  
 ccc ggg cta tgc tgc agt gag ttt tgt ctc ccg ggc gtc tgc ttc ggt 240  
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Leu Pro Gly Val Cys Phe Gly  
 65 70 75 80  
 ggt taactgcgct gatgtcttct actccctct gtgctacctg gcttgatctt 293  
 Gly  
 tgatcggcgt gtgcccttca ctggttatga acccactgat ottacctctc ttgaaggacc 353  
 tctgggggtcc agcatccaaa taagcgacat cccaatgaaa aaaaaaaaaa aaaaaaaaaa 412

<210> 152  
 <211> 81  
 <212> PRT  
 <213> Conus purpurascens

<400> 152

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

003221 496460

Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His  
 20 25 30

Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu  
 35 40 45

Asp Lys Lys Glu Ala Cys Tyr Ala Pro Gly Thr Phe Cys Gly Ile Lys  
 50 55 60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Leu Pro Gly Val Cys Phe Gly  
 65 70 75 80

Gly

<210> 153  
 <211> 29  
 <212> PRT  
 <213> Conus purpurascens

<220>  
 <221> SITE  
 <222> (1)..(29)  
 <223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at  
 residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su  
 lpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pr  
 o or hydroxy-Pro

<400> 153

Xaa Ala Cys Xaa Ala Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu  
 1 5 10 15

Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly  
 20 25

<210> 154  
 <211> 29  
 <212> PRT  
 <213> Conus purpurascens

<220>  
 <221> SITE  
 <222> (1)..(29)  
 <223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at  
 residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su  
 lpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pr  
 o or hydroxy-Pro

<400> 154

Xaa Ala Cys Xaa Ala Xaa Gly Thr Ala Cys Gly Ile Lys Xaa Gly Leu  
 1 5 10 15

Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly  
 20 25

008222" 2E96460

<210> 155  
 <211> 29  
 <212> PRT  
 <213> Conus purpurascens

<220>  
 <221> SITE  
 <222> (1)..(29)  
 <223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pro or hydroxy-Pro

<400> 155

Xaa Ala Cys Xaa Ala Xaa Gly Thr Phe Cys Gly Ala Lys Xaa Gly Leu  
 1 5 10 15

Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly  
 20 25

<210> 156  
 <211> 29  
 <212> PRT  
 <213> Conus purpurascens

<220>  
 <221> SITE  
 <222> (1)..(29)  
 <223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pro or hydroxy-Pro

<400> 156

Xaa Ala Cys Xaa Ala Xaa Gly Ala Phe Cys Gly Ile Lys Xaa Gly Leu  
 1 5 10 15

Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly  
 20 25

<210> 157  
 <211> 289  
 <212> DNA  
 <213> Conus magus

<220>  
 <221> CDS  
 <222> (1)..(252)

<400> 157  
 atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc acc 48  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr  
 1 5 10 15  
 tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu  
 20 25 30  
 ttt ccg aag gca cgt cat gaa atg aag aac cct gaa gcc tot aaa ttg 144

003327 7E967460

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
           35                    40                    45

aac aag aga gat ggg tgc tat aat gct ggt aca ttt tgt ggc atc cgt       192  
 Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg  
      50                    55                    60

cca gga ctc tgc tgc agc gag ttt tgc ttt tta tgg tgc ata aca ttt       240  
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe  
      65                    70                    75                    80

gtt gat tct ggc taacagtgtg cgttgggttag tgcctctcc tccccctc       289  
 Val Asp Ser Gly

<210> 158  
 <211> 84  
 <212> PRT  
 <213> Conus magus

<400> 158

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr  
   1                    5                    10                    15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu  
          20                    25                    30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
          35                    40                    45

Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg  
      50                    55                    60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe  
      65                    70                    75                    80

Val Asp Ser Gly

<210> 159  
 <211> 32  
 <212> PRT  
 <213> Conus magus

<220>  
 <221> SITE  
 <222> (1)..(32)  
 <223> Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,  
       O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or  
       hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu;  
       Xaa at residue 25 may be Trp or bromo-Trp

<400> 159

Asp Gly Cys Xaa Asn Ala Gly Thr Phe Cys Gly Ile Arg Xaa Gly Leu

008221 12200 4E964260

1                    5                    10                    15  
 Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Val Asp Ser  
                   20                    25                    30

<210> 160  
 <211> 273  
 <212> DNA  
 <213> Conus magus

<220>  
 <221> CDS  
 <222> (1)..(249)

<400> 160  
 atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc acc 48  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr  
 1                    5                    10                    15  
 tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu  
                   20                    25                    30  
 ttt ccg aag gca cgt cat gaa atg aag aac cct gaa gcc tct aaa ttg 144  
 Phe Pro Lys Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
                   35                    40                    45  
 aac aag aga gat gaa tgc tat cct cct ggt aca ttt tgt ggc atc aaa 192  
 Asn Lys Arg Asp Glu Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys  
                   50                    55                    60  
 cca gga ctt tgc tgc agc gcg ata tgc tta tcg ttt gtc tgc ata tca 240  
 Pro Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser  
 65                    70                    75                    80  
 ttt gat ttt tgattgatgt cttctcctcc cctc 273  
 Phe Asp Phe

<210> 161  
 <211> 83  
 <212> PRT  
 <213> Conus magus

<400> 161  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr  
 1                    5                    10                    15  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu  
                   20                    25                    30  
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
                   35                    40                    45  
 Asn Lys Arg Asp Glu Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys  
                   50                    55                    60  
 Pro Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser

003221 296460

80

[illegible]

<400> 164

Val Asp Ser Gly

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<220>
<221> SITE
<222> (1)..(32)
<223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
lpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or hydrox
y-Pro; Xaa at residue 25 may be Trp or bromo-Trp
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<400> 165

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<220>
<221> CDS
<222> (1) .. (249)
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48

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 tgg aca ttc gtc acg gct gat gac tcc aga tat gga ctg aag gat ctg 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asp Leu  
 20 25 30  
 ttt ccg aag gaa cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
 Phe Pro Lys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45  
 aac cag aga gaa gcc tgc tat aat gct ggt aca ttt tgt ggc atc aaa 192  
 Asn Gln Arg Glu Ala Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Lys  
 50 55 60  
 cca gga ctt tgc tgc agc gcg ata tgc tta tcg ttt gtc tgc ata tca 240  
 Pro Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser  
 65 70 75 80  
 ttt gat ttg attgatgtct tctcctcccc tc 271  
 Phe Asp Leu

<210> 167  
 <211> 83  
 <212> PRT  
 <213> Conus magus

<400> 167

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asp Leu  
 20 25 30  
 Phe Pro Lys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45  
 Asn Gln Arg Glu Ala Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Lys  
 50 55 60  
 Pro Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser  
 65 70 75 80

Phe Asp Leu

<210> 168  
 <211> 32  
 <212> PRT  
 <213> Conus magus  
 <220>  
 <221> SITE  
 <222> (1)..(32)  
 <223> Xaa at residue 1 may be Glu or gamma-carboxy-Glu; Xaa at residue

008227 "CE964260



4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or hydroxy-Pro

<400> 168

Xaa Ala Cys Xaa Asn Ala Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu  
1 5 10 15

Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser Phe Asp Phe  
20 25 30

<210> 169

<211> 272

<212> DNA

<213> Conus ermineus

<220>

<221> CDS

<222> (1)..(243)

<400> 169

atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg act gcc 48  
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aaa aat gga ctg gag aat cat 96  
Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His  
20 25 30

ttt tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg 144  
Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu  
35 40 45

gac aaa aag gaa gcc tgc tat ccg cct ggt act ttt tgt ggc ata aag 192  
Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys  
50 55 60

ccc ggg cta tgc tgc agt gag ttg tgt tta ccg gcc gtc tgc gtc ggt 240  
Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly  
65 70 75 80

ggt taactgccgt gatgtcttct cctccctc 272  
Gly

<210> 170

<211> 81

<212> PRT

<213> Conus ermineus

<400> 170

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His  
20 25 30

Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu  
35 40 45

0094963 12300

Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys  
 50 55 60

Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly  
 65 70 75 80

Gly

<210> 171  
 <211> 29  
 <212> PRT  
 <213> Conus ermineus

<220>  
 <221> SITE  
 <222> (1)..(29)  
 <223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at  
 residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su  
 lpho-Tyr or O-phospho-Tyr; Xaa at residues 5, 6, 14 and 24 may be  
 Pro or hydroxy-Pro

<400> 171

Xaa Ala Cys Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu  
 1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Xaa Ala Val Cys Val Gly  
 20 25

<210> 172  
 <211> 272  
 <212> DNA  
 <213> Conus purpurascens

<220>  
 <221> CDS  
 <222> (1)..(243)

<400> 172

atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg act gcc 48  
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aaa aat gga ctg gag aat cat 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His  
 20 25 30

ttt tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg 144  
 Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu  
 35 40 45

gac aaa aag gaa gcc tgc tat ccg cct ggt act ttt tgt ggc ata aag 192  
 Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys  
 50 55 60

ccc ggg cta tgc tgc agt gag ttg tgt tta ccg gcc gtc tgc gtc ggt 240  
 Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly

004493 "122800"

65

70

75

80

ggt taactgccgt gatgtcttct cctccctc  
Gly

272

<210> 173  
<211> 81  
<212> PRT  
<213> Conus purpurascens

<400> 173

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His  
20 25 30

Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu  
35 40 45

Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys  
50 55 60

Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly  
65 70 75 80

Gly

<210> 174  
<211> 29  
<212> PRT  
<213> Conus purpurascens

<220>  
<221> SITE  
<222> (1)..(29)  
<223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at  
residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su  
lpho-Tyr or O-phospho-Tyr; Xaa at residues 14 and 24 may be Pro o  
r hydroxy-Pro

<400> 174

Xaa Ala Cys Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu  
1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Xaa Ala Val Cys Val Gly  
20 25

<210> 175  
<211> 266  
<212> DNA  
<213> Conus striatus

09749637 122800



<212> PRT  
<213> Conus striatus

<220>  
<221> SITE  
<222> (1)..(31)  
<223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Trp or bromo-Trp

<400> 177

Xaa Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His Xaa Gly Leu  
1 5 10 15

Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Ile Asp  
20 25 30

<210> 178  
<211> 266  
<212> DNA  
<213> Conus striatus

<220>  
<221> CDS  
<222> (1)..(246)

<400> 178

atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc act 48  
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr  
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt 96  
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu  
20 25 30

ttt ccg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

aac aag aga gat ggg tgc tct agt ggt ggt aca ttt tgt ggc atc cat 192  
Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His  
50 55 60

cca gga ctc tgc tgc agc gag ttt tgc ttt ctt tgg tgc ata aca ttt 240  
Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe  
65 70 75 80

att gat tgatgtcttc tctcctccctc 266  
Ile Asp

<210> 179  
<211> 82  
<212> PRT  
<213> Conus striatus

<400> 179

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr  
1 5 10 15

003221" 2E96460

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu  
                   20                                  25                                  30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
                   35                                  40                                  45

Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His  
                   50                                  55                                  60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe  
                   65                                  70                                  75                                  80

Ile Asp

<210> 180

<211> 31

<212> PRT

<213> Conus striatus

<220>

<221> SITE

<222> (1)..(31)

<223> Xaa at residue 20 may be Glu or gamma-carboxy-Glu; Xaa at residue  
                   14 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Trp or br  
                   omo-Trp

<400> 180

Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His Xaa Gly Leu  
                   1                                  5                                  10                                  15

Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Ile Asp  
                   20                                  25                                  30

<210> 181

<211> 31

<212> PRT

<213> Conus striolatus

<220>

<221> SITE

<222> (1)..(31)

<223> Xaa at residues 6 and 14 may be Pro or hydroxy-Pro; Xaa at residu  
                   e 31 may be Glu or gamma-carboxy-Glu

<400> 181

Ser Lys Cys Phe Ser Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu  
                   1                                  5                                  10                                  15

Cys Cys Ser Val Arg Cys Phe Ser Leu Phe Cys Ile Ser Phe Xaa  
                   20                                  25                                  30

<210> 182

<211> 345

008227 122800

<212> DNA  
<213> Conus catus

<220>  
<221> CDS  
<222> (1)..(234)

<400> 182  
atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15  
  
tgg aca ttc gtc acg gct gat gac tcc aga aat gga ctg aag aat ctt 96  
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu  
20 25 30  
  
ttt ccg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45  
  
aac aag aga tat ggg tgc tct aat gct ggt gca ttt tgt ggc atc cat 192  
Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His  
50 55 60  
  
cca gga ctc tgc tgc agc gag ctt tgc ctg gtt tgg tgc aca 234  
Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Val Trp Cys Thr  
65 70 75  
  
tgagtgtctat tcttctggta cattttgtgg cttcaacgga ggactctgct gcagcaacct 294  
ttgcttattt tcgtgtgctt aacatttctgt gatgtcttct ctattccct c 345

<210> 183  
<211> 78  
<212> PRT  
<213> Conus catus

<400> 183  
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15  
  
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu  
20 25 30  
  
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45  
  
Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His  
50 55 60  
  
Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Val Trp Cys Thr  
65 70 75

<210> 184  
<211> 27  
<212> PRT  
<213> Conus catus

003221" 2E964760

<220>  
 <221> SITE  
 <222> (1)..(27)  
 <223> Xaa at residue 1 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 25 may be Trp or bromo-Trp

<400> 184

Xaa Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His Xaa Gly Leu  
 1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Val Xaa Cys Thr  
 20 25

<210> 185  
 <211> 345  
 <212> DNA  
 <213> Conus catus

<220>  
 <221> CDS  
 <222> (1)..(234)

<400> 185  
 atg aaa ctg acg tgt atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 tgg aca ttc gtc acg gct gat gaa tcc aga tat gga ctg aag aat ctt 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu  
 20 25 30  
 ttt ccg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45  
 aac aag aga tat ggg tgc tct aat gct ggt gca ttt tgt ggc atc cat 192  
 Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His  
 50 55 60  
 cca gga ctc tgc tgc agc gag ctt tgc ctg ggt tgg tgc aca 234  
 Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Gly Trp Cys Thr  
 65 70 75  
 tgagtgttat tctactggta cttttgtgg cttcaacgga ggactctgct gcagcaacct 294  
 ttgcttattt tcgtgtgctt aacatttcgt gatgtcttct ctattcccct c 345

<210> 186  
 <211> 78  
 <212> PRT  
 <213> Conus catus

<400> 186

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

008227 "CE954250



Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu  
20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His  
50 55 60

Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Gly Trp Cys Thr  
65 70 75

<210> 187

<211> 27

<212> PRT

<213> Conus catus

<220>

<221> SITE

<222> (1)..(27)

<223> Xaa at residue 1 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 25 may be Trp or bromo-Trp

<400> 187

Xaa Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His Xaa Gly Leu  
1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Gly Xaa Cys Thr  
20 25

<210> 188

<211> 266

<212> DNA

<213> Conus distans

<220>

<221> CDS

<222> (1)..(246)

<400> 188

atg aaa ctg acg tgt ctg atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctg 96  
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu  
20 25 30

tct ccg aag gca cct cac gaa atg aag aac ccc gaa gcc tct aaa tcg 144  
Ser Pro Lys Ala Pro His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser  
35 40 45

aac aag aga tat gag tgc tat ctc ctc gta cat ttt tgt ggc atc aac 192  
Asn Lys Arg Tyr Glu Cys Tyr Leu Leu Val His Phe Cys Gly Ile Asn  
50 55 60

008222" 4296460

ttt tcg tgatgtottc tctctccatc 266  
Phe Ser

<400> 189

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu  
20 25 30

Asn Lys Arg Tyr Glu Cys Tyr Leu Leu Val His Phe Cys Gly Ile Asn  
50 55 60

Phe Ser

 $\langle 220 \rangle$ 

<222> (1) .. (31)

<400> 190

Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser  
20 25 30

$\langle 210 \rangle$	191
$\langle 211 \rangle$	113
$\langle 212 \rangle$	DNA

<213> Conus regius

<220>

<221> CDS

<222> (1)..(93)

<400> 191

ttg	agc	aag	aga	gac	tgc	ctt	cct	gac	tac	acg	att	tgt	gcc	ttc	aat	48
Leu	Ser	Lys	Arg	Asp	Cys	Leu	Pro	Asp	Tyr	Thr	Ile	Cys	Ala	Phe	Asn	
1				5					10					15		

atg	ggt	ctg	tgc	tgc	agc	gac	aag	tgc	atg	ctc	gtc	tgc	ctg	ccg		93
Met	Gly	Leu	Cys	Cys	Ser	Asp	Lys	Cys	Met	Leu	Val	Cys	Leu	Pro		
			20					25					30			

tgatgtcttc	tcctcccctc	113
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<210> 192

<211> 31

<212> PRT

<213> Conus regius

<400> 192

Leu	Ser	Lys	Arg	Asp	Cys	Leu	Pro	Asp	Tyr	Thr	Ile	Cys	Ala	Phe	Asn
1				5					10					15	

Met	Gly	Leu	Cys	Cys	Ser	Asp	Lys	Cys	Met	Leu	Val	Cys	Leu	Pro
			20					25					30	

<210> 193

<211> 27

<212> PRT

<213> Conus regius

<220>

<221> SITE

<222> (1)..(27)

<223> Xaa at residues 5 and 27 may be Pro or hydroxy-Pro; Xaa at residue 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 193

Asp	Cys	Leu	Xaa	Asp	Xaa	Thr	Ile	Cys	Ala	Phe	Asn	Met	Gly	Leu	Cys
1				5					10					15	

Cys	Ser	Asp	Lys	Cys	Met	Leu	Val	Cys	Leu	Xaa
			20					25		

<210> 194

<211> 116

<212> DNA

<213> Conus regius

<220>

<221> CDS

<222> (1)..(96)

<400> 194

003001 493460

tgg	aca	ttc	gtc	acg	gct	gtg	cct	cac	tcc	agc	aat	gcg	ttg	gag	aat	96
Trp	Thr	Phe	Val	Thr	Ala	Val	Pro	His	Ser	Ser	Asn	Ala	Leu	Glu	Asn	
		20						25					30			

ctt tat ctg aag gca cat cat gaa atg aac aac ccc gaa gac tct gaa 144  
 Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu  
           35                          40                          45

ttg aac aag agg tgc tat gat ggt ggg aca ggt tgt gac tct gga aac 192  
 Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn  
           50                          55                          60

caa tgc tgc agt ggc tgg tgc att ttc gcc tgc ctc taaaactgtc 238  
 Gln Cys Cys Ser Gly Trp Cys Ile Phe Ala Cys Leu  
           65                          70                          75

gtgatgtctt ctctctccct c 259

<210> 198  
 <211> 76  
 <212> PRT  
 <213> Conus gloriamaris

<400> 198

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1                          5                          10                          15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn  
           20                          25                          30

Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu  
           35                          40                          45

Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn  
           50                          55                          60

Gln Cys Cys Ser Gly Trp Cys Ile Phe Ala Cys Leu  
 65                          70                          75

<210> 199  
 <211> 24  
 <212> PRT  
 <213> Conus gloriamaris

<220>  
 <221> SITE  
 <222> (1)..(24)  
 <223> Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,  
           r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or  
           bromo-Trp

<400> 199

Cys Xaa Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn Gln Cys Cys Ser  
 1                          5                          10                          15

Gly Xaa Cys Ile Phe Ala Cys Leu  
           20

003221" 4696460

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<220>
<221> CDS
<222> (1) .. (228)
```

```
<210> 201
<211> 76
<212> PRT
<213> Conus dalli
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<210> 202
<211> 24
<212> PRT
<213> Conus dalli
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<400> 202

Gly Xaa Cys Ile Phe Val Cys Leu  
20

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<220>
<221> CDS
<222> (1) .. (228)
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tgg aca gtc gtc acg gct gtg cct cac tcc aac aag cgg ttg gcg aat 96  
 Trp Thr Val Val Thr Ala Val Pro His Ser Asn Lys Arg Leu Ala Asn  
 20 25 30

ctt tat ctg aag gca cgt cac gaa atg aaa aac ccc gaa gcc tct aat 144  
Leu Tyr Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Asn  
35 40 45

gtg gac aag agg tgc ttt gag agt tgg gta gct tgt gag tct cca aaa 192  
Val Asp Lys Arg Cys Phe Glu Ser Trp Val Ala Cys Glu Ser Pro Lys  
50 55 60

cga tgc tgc agt cac gtg tgc ctt ttc gtc tgc acc tgaaactgcc 238  
Arg Cys Cys Ser His Val Cys Leu Phe Val Cys Thr  
65 70 75

gtgatgtctt ctctccct c 259

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<210> 204
<211> 76
<212> PRT
<213> Conus pennaceus
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<400> 204

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Val Val Thr Ala Val Pro His Ser Asn Lys Arg Leu Ala Asn  
20 25 30





253

<400> 207

<400> 208

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<220>
<221> CDS
<222> (1)..(228)
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48

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<210> 210
<211> 76
<212> PRT
<213> Conus ammiralis
```

Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu  
35 40 45

Gln Cys Cys Ser Gly Trp Cys Ile Phe Leu Cys Leu  
65 70 75

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<220>
<221> SITE
<222> (1)..(24)
<223> Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or
bromo-Trp
```

Cys Xaa Asp Gly Gly Thr Ser Cys Asr Thr Gly Asn Gln Cys Cys Ser  
1 5 10 15

Gln Cys Cys Ser Gly Trp Cys Ile Phe Val Ser Cys Leu  
65 70 75

<400> 216

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu  
20 25 30

Phe Ser Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu  
35 40 45

Glu Lys Arg Asp Cys Gln Ala Leu Trp Asp Tyr Cys Pro Val Pro Leu  
50 55 60

Leu Ser Ser Gly Asp Cys Cys Tyr Gly Leu Ile Cys Gly Pro Phe Val  
65 70 75 80

Cys Ile Gly Trp

<210> 217  
<211> 33  
<212> PRT  
<213> Conus gloriamaris

<220>  
<221> SITE  
<222> (1)..(33)  
<223> Xaa at residues 6 and 33 may be Trp or bromo-Trp; Xaa at residues  
8 and 21 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su  
lpho-Tyr or O-phospho-Tyr; Xaa at residues 10, 12 and 27 may be P  
ro or hydroxy-Pro

<400> 217

Asp Cys Gln Ala Leu Xaa Asp Xaa Cys Xaa Val Xaa Leu Leu Ser Ser  
1 5 10 15

Gly Asp Cys Cys Xaa Gly Leu Ile Cys Gly Xaa Phe Val Cys Ile Gly  
20 25 30

Xaa

<210> 218  
<211> 275  
<212> DNA  
<213> Conus omaria

<220>  
<221> CDS  
<222> (1)..(249)

<400> 218  
atg aaa ctg acg tgc ctg atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15  
tgg aca ttc gtc atg gct gat gac tcc aac aat gga ctg gca aat ctt 96

000222T 22364260



Glu Lys Lys Asp Cys Gln Glu Lys Trp Asp Tyr Cys Pro Val Pro Phe  
50 55 60

Leu Gly Ser Arg Tyr Cys Cys Asp Gly Phe Ile Cys Pro Ser Phe Phe  
65 70 75 80

Cys Ala

<210> 223  
<211> 31  
<212> PRT  
<213> Conus dalli

<220>  
<221> SITE  
<222> (1)..(31)  
<223> Xaa at residue 4 may be Glu or gamma-carboxy-Glu; Xaa at residue 6 may be Trp or bromo-Trp; Xaa at residues 8 and 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 10, 12 and 26 may be Pro or hydroxy-Pro

<400> 223

Asp Cys Gln Xaa Lys Xaa Asp Xaa Cys Xaa Val Xaa Phe Leu Gly Ser  
1 5 10 15

Arg Xaa Cys Cys Asp Gly Phe Ile Cys Xaa Ser Phe Phe Cys Ala  
20 25 30

<210> 224  
<211> 271  
<212> DNA  
<213> Conus dalli

<220>  
<221> CDS  
<222> (1)..(252)

<400> 224

atg aaa ctg acg tgc gtg atg atc gtt gct gtg ttg ttc ctg aca gcc 48  
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

tgg acg cta gtc atg gct gat gac tcc aac aat gga ctg gcg aat cat 96  
Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn His  
20 25 30

ttt tgg aaa tca cgt gac gaa atg gag gac cct gaa gct tct aaa ttg 144  
Phe Trp Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu  
35 40 45

gag aaa agg gat tgc caa ggc gaa tgg gag ttt tgt ata gta ccg gtc 192  
Glu Lys Arg Asp Cys Gln Gly Glu Trp Glu Phe Cys Ile Val Pro Val  
50 55 60

ctt gga ttt gtg tat tgc tgc ccc tgg ctt atc tgt ggc cct ttc gtc 240  
Leu Gly Phe Val Tyr Cys Cys Pro Trp Leu Ile Cys Gly Pro Phe Val  
65 70 75 80

tgc gtt gat atc tgatgtcttc tatccccctc 271  
Cys Val Asp Ile

000224 25967460



<210> 225  
 <211> 84  
 <212> PRT  
 <213> Conus dalli

<400> 225

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn His  
 20 25 30

Phe Trp Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu  
 35 40 45

Glu Lys Arg Asp Cys Gln Gly Glu Trp Glu Phe Cys Ile Val Pro Val  
 50 55 60

Leu Gly Phe Val Tyr Cys Cys Pro Trp Leu Ile Cys Gly Pro Phe Val  
 65 70 75 80

Cys Val Asp Ile

<210> 226  
 <211> 33  
 <212> PRT  
 <213> Conus dalli

<220>  
 <221> SITE  
 <222> (1)..(33)  
 <223> Xaa at residues 5 and 7 may be Glu or gamma-carboxy-Glu; Xaa at r  
 esidues 6 and 22 may be Trp or bromo-Trp; Xaa at residues 12, 21  
 and 27 may be Pro or hydroxy-Pro;

<220>  
 <221> SITE  
 <222> (1)..(33)  
 <223> Xaa at residue 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-T  
 yr, O-sulpho-Tyr or O-phospho-Tyr

<400> 226

Asp Cys Gln Gly Xaa Xaa Xaa Phe Cys Ile Val Xaa Val Leu Gly Phe  
 1 5 10 15

Val Xaa Cys Cys Xaa Xaa Leu Ile Cys Gly Xaa Phe Val Cys Val Asp  
 20 25 30

Ile

00822T 2E964650

$\langle 220 \rangle$   
 $\langle 221 \rangle$  CDS  
 $\langle 222 \rangle$  (1) .. (234)

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<210> 228
<211> 78
<212> PRT
<213> Conus pennaceus
```

```
<210> 229
<211> 31
<212> PRT
<213> Conus pennaceus
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<400> 229

Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Xaa Gln  
20 25 30

```
<220>
<221> CDS
<222> (122) .. (229)
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<210>	231
<211>	36
<212>	PRT
<213>	Conus marmoreus

Asn Glu Arg Asp Cys Leu Asn Val Asp Tyr Phe Cys Gly Ile Pro Phe  
1 5 10 15

Val Asn Asn Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr  
20 25 30



Ile Ala Gln Arg Phe Lys Thr Val  
35 40

```

<210> 235
<211> 36
<212> PRT
<213> Conus marmoreus

<220>
<221> SITE
<222> (1)..(36)
<223> Xaa at residues 1 and 4 may be Glu or gamma-carboxy-Glu; Xaa at r
esidues 7 and 8 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr
, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 12 may be Pro or
hydroxy-Pro

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```

<400> 235
Xaa Cys Leu Xaa Ala Asp Xaa Xaa Cys Val Leu Xaa Phe Val Gly Asn
1          5          10          15
Gly Met Cys Cys Ser Gly Ile Cys Val Phe Val Cys Ile Ala Gln Arg
          20          25          30
Phe Lys Thr Val
          35

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<210> 236
<211> 525
<212> DNA
<213> Conus marmoreus
```

```
<220>
<221> CDS
<222> (131) .. (241)
```

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<400> 236
gtaccgggtcc ggaattcccg ggtcgacatc atcatcatcg atccatctgt ccatccatcc 60

atccattcat tcattcgctg ccaaactgtc ataaacattt gagtctctct ttctgttttt 120

atctgacaga ttg aac gag aga gac tgc ctt gaa cct gat tat gtt tgc 169
          Leu Asn Glu Arg Asp Cys Leu Glu Pro Asp Tyr Val Cys
          1                      5                      10

ggc ata ccg ttt gtg ttc aac ggg cta tgc tgc agt gga att tgt gtt 217
Gly Ile Pro Phe Val Phe Asn Gly Leu Cys Cys Ser Gly Ile Cys Val
          15                      20                      25

ttt atc tgc ata gcc caa aag tat taaaacgccg tgatgtcttc tattcccatc 271
Phe Ile Cys Ile Ala Gln Lys Tyr
30                      35

tagtagtagt aggcggccgc tctagaggat ccaagcttac gtacgcgtgc atgcgacgtc 331

```



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<210> 240
<211> 34
<212> PRT
<213> Conus marmoreus
```

Glu Lys Arg Ala Cys Ser Lys Lys Trp Glu Tyr Cys Ile Val Pro Ile  
1 5 10 15

Cys Val

<210>	241
<211>	31
<212>	PRT
<213>	Conus marmoreus

```
<220>
<221> SITE
<222> (1)..(31)
<223> Xaa at residue 6 may be Trp or bromo-Trp; Xaa at residue 7 may be
      Glu or gamma-carboxy-Glu; Xaa at residues 8 and 18 may be Tyr, 1
      25-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T
      yr; Xaa at residues 12, 21 and 27 may be Pro or hydroxy-Pro
```

Ala Cys Ser Lys Lys Xaa Xaa Xaa Cys Ile Val Xaa Ile Leu Gly Phe  
1 5 10 15

Val Xaa Cys Cys Xaa Gly Leu Ile Cys Gly Xaa Phe Val Cys Val  
                   20                  25                  30

<210> 242  
 <211> 552  
 <212> DNA  
 <213> Conus omaria

<220>  
 <221> CDS  
 <222> (149)..(271)

<400> 242  
 aaagccggtg cgcctgcagg taccggtcgg gaattcccgg gtcgacatca tcatcatcat 60  
 cgatccatct gtccatccat ccattcattc attcactgcc aaactgtcat aaatatttga 120  
 gtctctcttt ctgtttttat ctgacaga ttg aac gag aga gac tgc ott aat 172  
                                   1                                  5  
                                   Leu Asn Glu Arg Asp Cys Leu Asn  
 gtt gat tat ttt tgt ggc ata ccg ttt gtg aac aac ggg cta tgc tgc 220  
 Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Asn Asn Gly Leu Cys Cys  
           10                  15                  20  
 agt ggc aat tgt gtt ttt tgt ctg cac acc cca agg gaa gta aaa ctg 268  
 Ser Gly Asn Cys Val Phe Cys Leu His Thr Pro Arg Glu Val Lys Leu  
   25                  30                  35                  40  
 ccg tgatgtcttc ttttcccttc tagtagtagt aggcggccgc tctagaggat 321  
 Pro  
 ccaagcttac gtacgcgtgc atgcgacgtc atagctcttc tatagtgtca cctaaattca 381  
 attcactggc cgtcgtttta caacgtcgtg actgggaaaa ccttggcggtt acccaactta 441  
 atcgccttgc agcacatccc cctttcgcca gctggcgtaa tagcgaagag gcccgccaccg 501  
 atcgcccttc ccaacagttg cgcagcctga atggcgaatg ggacgcgccc t 552

<210> 243  
 <211> 41  
 <212> PRT  
 <213> Conus omaria

<400> 243

Leu Asn Glu Arg Asp Cys Leu Asn Val Asp Tyr Phe Cys Gly Ile Pro  
 1                  5                  10                  15

Phe Val Asn Asn Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Cys Leu  
           20                  25                  30

His Thr Pro Arg Glu Val Lys Leu Pro  
       35                  40

<210> 244  
 <211> 37  
 <212> PRT

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<223> Xaa at residue 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 12, 31 and 37 may be Pro or hydroxy-Pro; Xaa at residue 33 may be Glu or gamma-carboxy-Glu

<211> 28



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<220>
<221> SITE
<222> (1)..(32)
<223> Xaa at residues 4 and 7 may be Glu or gamma-carboxy-Glu; Xaa at r
        esidue 12 may be Pro or hydroxy-Pro

```

Asp Cys His Xaa Val Gly Xaa Phe Cys Gly Leu Xaa Leu Ile Lys Asn  
1 5 10 15

Gly Leu Cys Cys Ser Gln Ile Cys Leu Gly Val Cys Ala Lys Val Phe  
20 25 30

```
<220>
<221> CDS
<222> (2)..(100)
```

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<400> 251
a tta gac aag aaa gag tgc act gcc aat ggt gaa ttt tgt ggc ata tcg      49
Leu Asp Lys Lys Glu Cys Thr Ala Asn Gly Glu Phe Cys Gly Ile Ser
 1          5          10          15

gtc ttt gga agc tac cta tgc tgc agt ggc cgg tgt gta ttc gtc tgc      97
Val Phe Gly Ser Tyr Leu Cys Cys Ser Gly Arg Cys Val Phe Val Cys
          20          25          30

atc tagttgaact gccgtgatgt cttctactcc cct      133
Ile

```

<400> 252

Val Phe Gly Ser Tyr Leu Cys Cys Ser Gly Arg Cys Val Phe Val Cys  
20 25 30

```
<210> 253
<211> 29
<212> PRT
<213> Conus radiatus
```

<220>  
 <221> SITE  
 <222> (1)..(29)  
 <223> Xaa at residues 1 and 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 17 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 253

Xaa Cys Thr Ala Asn Gly Xaa Phe Cys Gly Ile Ser Val Phe Gly Ser  
 1 5 10 15

Xaa Leu Cys Cys Ser Gly Arg Cys Val Phe Val Cys Ile  
 20 25

<210> 254  
 <211> 133  
 <212> DNA  
 <213> Conus radiatus

<220>  
 <221> CDS  
 <222> (2)..(100)

<400> 254

a ttg gac aag aaa gag tgc act acc aat ggt gaa ttt tgt ggc ata tcg 49  
 Leu Asp Lys Lys Glu Cys Thr Thr Asn Gly Glu Phe Cys Gly Ile Ser  
 1 5 10 15

gtc ttt gca agc ttc cta tgc tgc agt ggc ctg tgt gta ttc gtc tgc 97  
 Val Phe Ala Ser Phe Leu Cys Cys Ser Gly Leu Cys Val Phe Val Cys  
 20 25 30

atc tagctgaact gccgtgatgt cttctcttcc cct 133  
 Ile

<210> 255  
 <211> 33  
 <212> PRT  
 <213> Conus radiatus

<400> 255

Leu Asp Lys Lys Glu Cys Thr Thr Asn Gly Glu Phe Cys Gly Ile Ser  
 1 5 10 15

Val Phe Ala Ser Phe Leu Cys Cys Ser Gly Leu Cys Val Phe Val Cys  
 20 25 30

Ile

<210> 256  
 <211> 29  
 <212> PRT  
 <213> Conus radiatus

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<220>
<221> SITE
<222> (1) .. (29)
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<400> 259

Xaa   Leu   Cys   Cys   Ser   Gly   Arg   Cys   Ile   Phe   Val   Cys   Val  
                    20                                    25

```
<220>
<221> CDS
<222> (1)..(99)
```

ata att gga gcg ttt ctg tgc tgt agt ggc tac tgc ctt gtc gtc tgc	96
Ile Ile Gly Ala Phe Leu Cys Cys Ser Gly Tyr Cys Leu Val Val Cys	
20 25 30	

```
<210> 261
<211> 33
<212> PRT
<213> Conus regius
```

Leu Asn Lys Arg Ser Cys Leu Pro Leu Asp Trp Phe Cys Gly Phe Asn  
1 5 10 15

Met

```
<220>
<221> SITE
<222> (1)..(29)
<223> Xaa at residue 4 may be Pro or hydroxy-Pro; Xaa at residue 7 may
```

<400> 262

Phe Leu Cys Cys Ser Gly Xaa Cys Leu Val Val Cys Met  
20 25

<213> Conus delessertii

<222> (1) .. (285)

tgataaaagct gccttqatgt cttctcctcc cctc 319

<213> Conus delessertii

<400> 264

Cys Gln Phe Ile Val Ala Gly Asp Ser Ser Asp Gly Gln Glu Asn Pro  
20 25 30

```

<400> 266
gctgggttcgc ctgcaggtac cggtcgga tccccgggtc gacatcatca tcatcgatcc 60
atctgtccat ccattctattc attcattcat tcgctgccaa actgtattaa atattcaagt 120
ctctctttct gtttgtgtct aacaga ttg aga tgg tgc att cct agt ggt gaa 173
Leu Arg Trp Cys Ile Pro Ser Gly Glu
1 5
ctt tgt ttc cgc tcg gat cac ata gga tgc tgc agt ggc aag tgc gca 221
Leu Cys Phe Arg Ser Asp His Ile Gly Cys Cys Ser Gly Lys Cys Ala

```



10 15 20 25  
 ttc gtc tgc ttg taaaactgcc gtgatgtctt ctctcccat ctagtagtag 273  
 Phe Val Cys Leu

taggcggccg ctctagagga tccaagctta cgtacgcgtg catgcgacgt catagctctt 333  
 ctatagtgtc acctaaattc aattcactgg ccgtcgtttt acaacgtcgt gactgggaaa 393  
 accctggcgt tacccaactt aatcgcttg cagcacatcc ccctttcgcc agctggcgta 453  
 atagcgaaga ggcccgacc gatcgccctt cccaacagtt tgccgagcct gaatggcgaa 513  
 tgggacgcgc cctgtagcgg cgcattaaac cgcggcgggt gtgggtgggt tacgcccacg 573  
 tgaccgccta cacttgccag cgcctanag ccccgctcct ttcgctttct tcccttctt 633  
 ttctcgnac gtttcggccg nttttcccg tcaagctctt aaatcggggg gcttcccttt 693  
 aagggttncc gaattantgc tttaccgna cccttgaccc ccaaaaaaac ttggantaag 753  
 gggngatggn tcncgtaant gggggccatc nccctgaan agaacggtt ttonccctt 813  
 ttgacngttg gnggttcnc ggtttttaa aaangggacc tttntttcc aaaactggga 873  
 ananacctaa accctatatt tggggctatt ttttgantt tnaaanggga ttttgcccca 933  
 ttttnggcc tnttgggta aaaaaaagag ccggttttaa aaaaaattt accccaaatt 993  
 ttaacaaaaa tttttt 1009

<210> 267  
 <211> 29  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> misc\_feature  
 <222> (1)..(1009)  
 <223> n may be any nucleotide

<400> 267

Leu Arg Trp Cys Ile Pro Ser Gly Glu Leu Cys Phe Arg Ser Asp His  
 1 5 10 15

Ile Gly Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu  
 20 25

<210> 268  
 <211> 29  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> SITE  
 <222> (1)..(29)  
 <223> Xaa at residue3 may be Trp or bromo-Trp; Xaa at residue 6 may be  
 Pro or hydroxy-Pro; Xaa at residue 9 may be Glu or gamma-carboxy  
 -Glu

Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu  
20 25

<210> 272  
 <211> 90  
 <212> DNA  
 <213> Conus striatus

<220>  
 <221> CDS  
 <222> (1)..(87)

<400> 272  
 ttg aga tgg tgc att cct agt ggt gat ctt tgt ttc cgc tcg gat cac 48  
 Leu Arg Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Arg Ser Asp His  
 1 5 10 15  
 ata caa tgc tgc agt ggc aag tgc gca ttc gtc tgc ttg taa 90  
 Ile Gln Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu  
 20 25

<210> 273  
 <211> 29  
 <212> PRT  
 <213> Conus striatus

<400> 273  
 Leu Arg Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Arg Ser Asp His  
 1 5 10 15

Ile Gln Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu  
 20 25

<210> 274  
 <211> 27  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> SITE  
 <222> (1)..(27)  
 <223> Xaa at residue may be Trp or bromo-Trp; Xaa at residue 4 may be  
 Pro or hydroxy-Pro

<400> 274  
 Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Arg Ser Asp His Ile Gln  
 1 5 10 15  
 Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu  
 20 25

<210> 275  
 <211> 206  
 <212> DNA  
 <213> Conus obscurus

<220>  
 <221> CDS  
 <222> (77)..(175)

<400> 275

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<220>
<221> CDS
<222> (22) .. (117)
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ggatcttgca cggtgaattt cgcttcatat ttttctactg tcgtcttttg catcatccaa 60

aacatcacca ag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc 111  
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe  
 1 5 10

ttg acc gcc tgg aca ttc gtc acg gct gtg cct cac tcc agc gat gta 159  
 Leu Thr Ala Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val  
 15 20 25

ttg gag aat ctt tat ctg aag gca ctt cac gaa acg gaa aac cac gaa 207  
 Leu Glu Asn Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu  
 30 35 40 45

gcc tct aaa ttg aac gtg aga gac gac gag tgc gaa cct cct gga gat 255  
 Ala Ser Lys Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp  
 50 55 60

ttt tgt ggc ttt ttt aaa att ggg ccg cct tgc tgc agt ggc tgg tgc 303  
 Phe Cys Gly Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys  
 65 70 75

ttc ctc tgg tgc gcc taaaactgcc gtgatgtctt ctattcccoct ctgtgctacc 358  
 Phe Leu Trp Cys Ala  
 80

tggcttgatc tttgattggc gcgtgccctt cagtgggtat gaacccccct gagccgactc 418

tctggggggc tcgggggggtc aacatccaaa taaagcgaca acacaatcac aagtaaaaaa 478

<210> 282

<211> 82

<212> PRT

<213> Conus geographus

<400> 282

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val Leu Glu Asn  
 20 25 30

Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys  
 35 40 45

Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly  
 50 55 60

Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp  
 65 70 75 80

Cys Ala

<210> 283

<211> 30

<212> PRT

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<221> misc feature

ttc gtc acg gct gtt gac tcc aaa aat gaa ctg gag aac aga gga gga 153  
Phe Val Thr Ala Val Asp Ser Lys Asn Glu Leu Glu Asn Arg Gly Gly  
20 25 30





<400> 289

Phe Cys Cys Lys Gly Xaa Cys Leu Phe Val Cys Ile Ser  
20 25

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<220>
<221> CDS
<222> (1)..(246)
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```
<210> 291
<211> 82
<212> PRT
<213> Conus leopardus
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Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Ile Phe Ile Thr Ala Asp Asp Ser Thr Asn Gly Leu Glu Asn Arg  
20 25 30

aac tgc tgc tat acc tat tgc ttt att gta gtc tgc cta taaaactacc 241

<220>  
<221> CDS

&lt;222&gt; (7)..(240)

&lt;400&gt; 296

ggatcc atg aaa ctg acg tgt atg gtg atc gtt gct gtg cta ttc ttg 48  
 Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu  
 1 5 10

acc gcc tcg gct gat gac tcc aga aat gga ttc gag aat cga aat gga 96  
 Thr Ala Ser Ala Asp Asp Ser Arg Asn Gly Phe Glu Asn Arg Asn Gly  
 15 20 25 30

gaa cga aac gaa aac gaa atg aag aac ctc gaa gcc tct aaa ttg aac 144  
 Glu Arg Asn Glu Asn Glu Met Lys Asn Leu Glu Ala Ser Lys Leu Asn  
 35 40 45

agg aga gac ggc gat tgc gtt gat ggt ggt gaa ttt tgt ggc ttt ccg 192  
 Arg Arg Asp Gly Asp Cys Val Asp Gly Gly Glu Phe Cys Gly Phe Pro  
 50 55 60

aaa att gga ggg cca tgc tgt agt ggc tgg tgc ttt ttc gtc tgc tta 240  
 Lys Ile Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu  
 65 70 75

taaaactgcc atgatgtctt ctacccccct ctgtgctacc tgacttgatc tttgattggc 300

gtgtgccctt cactgggttat gaacccctct gatccgactc tctggaggcc tcgggggtcc 360

aacatccaaa taaagcgaca gcaaaaaaaaa aaaaaaaaaa aa 402

&lt;210&gt; 297

&lt;211&gt; 78

&lt;212&gt; PRT

&lt;213&gt; Conus quercinus

&lt;400&gt; 297

Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Ser Ala Asp Asp Ser Arg Asn Gly Phe Glu Asn Arg Asn Gly Glu Arg  
 20 25 30

Asn Glu Asn Glu Met Lys Asn Leu Glu Ala Ser Lys Leu Asn Arg Arg  
 35 40 45

Asp Gly Asp Cys Val Asp Gly Gly Glu Phe Cys Gly Phe Pro Lys Ile  
 50 55 60

Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu  
 65 70 75

&lt;210&gt; 298

&lt;211&gt; 30

&lt;212&gt; PRT

&lt;213&gt; Conus quercinus

&lt;220&gt;

&lt;221&gt; SITE

00822T 4E96460

<400> 300

acc gcc tgg aca ttc gtc acg gct gac tcc ata cgt gca ctg gag gat 96  
Thr Ala Trp Thr Phe Val Thr Ala Asp Ser Ile Arg Ala Leu Glu Asp

15	20	25	30	
ttt ttt gcg aag gca cgt gac gaa atg gaa aac agc gga gct tct cca				144
Phe Phe Ala Lys Ala Arg Asp Glu Met Glu Asn Ser Gly Ala Ser Pro	35	40	45	
ttg aac gag aga gac tgc cga cct gta ggt caa tat tgt ggc ata ccg				192
Leu Asn Glu Arg Asp Cys Arg Pro Val Gly Gln Tyr Cys Gly Ile Pro	50	55	60	
tat aag cac aac tgg cga tgc tgc agt cag ctt tgt gca att atc tgt				240
Tyr Lys His Asn Trp Arg Cys Cys Ser Gln Leu Cys Ala Ile Ile Cys	65	70	75	
gtt tcc taacccctct gatcctactc tctgaagacc tccgggattc aacatccaaa				296
Val Ser	80			
taaagcgaca tcccgatnaa aaaaaangaa aaaaaaaaaa aaaa				340

<210> 303  
 <211> 80  
 <212> PRT  
 <213> Conus arenatus

<220>  
 <221> misc feature  
 <222> (1)..(340)  
 <223> n may be any nucleotide

<400> 303

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala			
1 5 10 15			

Trp Thr Phe Val Thr Ala Asp Ser Ile Arg Ala Leu Glu Asp Phe Phe			
20 25 30			

Ala Lys Ala Arg Asp Glu Met Glu Asn Ser Gly Ala Ser Pro Leu Asn			
35 40 45			

Glu Arg Asp Cys Arg Pro Val Gly Gln Tyr Cys Gly Ile Pro Tyr Lys			
50 55 60			

His Asn Trp Arg Cys Cys Ser Gln Leu Cys Ala Ile Ile Cys Val Ser			
65 70 75 80			

<210> 304  
 <211> 30  
 <212> PRT  
 <213> Conus arenatus

<220>  
 <221> SITE  
 <222> (1)..(30)  
 <223> Xaa at residues 4 and 12 may be Pro or hydroxy-Pro; Xaa at residues 8 and 13 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 17 may be Trp or brom

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o-Trp

&lt;400&gt; 304

Asp Cys Arg Xaa Val Gly Gln Xaa Cys Gly Ile Xaa Xaa Lys His Asn  
 1 5 10 15  
 Xaa Arg Cys Cys Ser Gln Leu Cys Ala Ile Ile Cys Val Ser  
 20 25 30

&lt;210&gt; 305

&lt;211&gt; 281

&lt;212&gt; DNA

&lt;213&gt; Conus arenatus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (7)..(234)

&lt;400&gt; 305

ggatcc atg aaa ctg acg tgt gtg gtg atc gtt gtt gtg ctg ttc ttg 48  
 Met Lys Leu Thr Cys Val Val Ile Val Val Val Leu Phe Leu  
 1 5 10  
 acc gcc tgg aca ttc gtc aag gct gat gac tcc ata aat gga ttg gag 96  
 Thr Ala Trp Thr Phe Val Lys Ala Asp Asp Ser Ile Asn Gly Leu Glu  
 15 20 25 30  
 aat ctt ttt ccg aag gca cgt cac gaa atg aag aac ccc gaa gcc tct 144  
 Asn Leu Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser  
 35 40 45  
 aaa ttg aac gag agg tgc ctt gaa aag ggt gta ctt tgt gat ccg agt 192  
 Lys Leu Asn Glu Arg Cys Leu Glu Lys Gly Val Leu Cys Asp Pro Ser  
 50 55 60  
 gct gga aac tgc tgt agt ggc gaa tgc gtt tta gtc tgc ctc 234  
 Ala Gly Asn Cys Cys Ser Gly Glu Cys Val Leu Val Cys Leu  
 65 70 75  
 taaaactacc gtgatgtctt ctactcccat ctgtgctacc cctcgag 281

&lt;210&gt; 306

&lt;211&gt; 76

&lt;212&gt; PRT

&lt;213&gt; Conus arenatus

&lt;400&gt; 306

Met Lys Leu Thr Cys Val Val Ile Val Val Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Trp Thr Phe Val Lys Ala Asp Asp Ser Ile Asn Gly Leu Glu Asn Leu  
 20 25 30  
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45  
 Asn Glu Arg Cys Leu Glu Lys Gly Val Leu Cys Asp Pro Ser Ala Gly

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60

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<210> 309
<211> 78
<212> PRT
<213> Conus arenatus
```

gat aga ggc ata tgg ggg gaa cct ttg tcg aag gca cgt gac gaa atg 144  
Asp Arg Gly Ile Trp Gly Glu Pro Leu Ser Lys Ala Arg Asp Glu Met

35 40 45  
 aac ccc gaa gtc tct aaa cgg gat tgc tgg cct caa tat tgg ttt tgt 192  
 Asn Pro Glu Val Ser Lys Arg Asp Cys Trp Pro Gln Tyr Trp Phe Cys  
 50 55 60  
 ggc cta cag agg gga tgc tgc cca ggg act act tgc ttc ttc ctt tgc 240  
 Gly Leu Gln Arg Gly Cys Cys Pro Gly Thr Thr Cys Phe Phe Leu Cys  
 65 70 75  
 ttt tagtgatctc ttgactccc ttctgtgcta cctggcttga cctttgattg 293  
 Phe  
 gcgcgtgccc ttacttggtt ataaaccct ctgttctcc tctctggacg cttcggggtg 353  
 tccagcatcc aaataaagcg acgtcccca aaaaaaaaa aaaaaaa 400

<210> 312  
 <211> 79  
 <212> PRT  
 <213> Conus tessulatus

<400> 312

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Met Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Ile Thr Ala Asp Asp Ser Ile Asn Gly Leu Glu Asp Arg  
20 25 30

Gly Ile Trp Gly Glu Pro Leu Ser Lys Ala Arg Asp Glu Met Asn Pro  
35 40 45

Glu Val Ser Lys Arg Asp Cys Trp Pro Gln Tyr Trp Phe Cys Gly Leu  
50 55 60

Gln Arg Gly Cys Cys Pro Gly Thr Thr Cys Phe Phe Leu Cys Phe  
65 70 75

<210> 313  
 <211> 26  
 <212> PRT  
 <213> Conus tessulatus

<220>  
 <221> SITE  
 <222> (1)..(26)  
 <223> Xaa at residues 3 and 7 may be Trp or bromo-Trp; Xaa at residues  
 4 and 17 may be Pro or hydroxy-Pro; Xaa at residue 6 may be Tyr,  
 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-  
 Tyr

<400> 313

Asp Cys Xaa Xaa Gln Xaa Xaa Phe Cys Gly Leu Gln Arg Gly Cys Cys  
1 5 10 15

Xaa Gly Thr Thr Cys Phe Phe Leu Cys Phe  
20 25

<210> 314  
<211> 419  
<212> DNA  
<213> Conus tessulatus

<220>  
<221> CDS  
<222> (7)..(249)

<400> 314  
ggatcc atg aaa ctg acg tgc gtg gtg gtc gtt gct gtg ctg ttc ttg 48  
Met Lys Leu Thr Cys Val Val Val Val Ala Val Leu Phe Leu  
1 5 10

aac gcc tgg aca ttc gcc acg gct gtt gac tcc aaa cat gca ctg gcg 96  
Asn Ala Trp Thr Phe Ala Thr Ala Val Asp Ser Lys His Ala Leu Ala  
15 20 25 30

aaa ctt ttt atg aag gca cgt gac gaa atg tat aac ccc gat gcc act 144  
Lys Leu Phe Met Lys Ala Arg Asp Glu Met Tyr Asn Pro Asp Ala Thr  
35 40 45

aaa ttg gac gat aag aga tgg tgc gct tta gat ggt gaa ctt tgt atc 192  
Lys Leu Asp Asp Lys Arg Trp Cys Ala Leu Asp Gly Glu Leu Cys Ile  
50 55 60

ata ccg gtc att ggg tcc ata ttt tgc tgc cat ggc ata tgt atg atc 240  
Ile Pro Val Ile Gly Ser Ile Phe Cys Cys His Gly Ile Cys Met Ile  
65 70 75

tac tgc gtc tagttgaact gccgtgatgt cttctactcc cctctgtgct 289  
Tyr Cys Val  
80

acccttggtt tgatctttga ttgccctgtg cccttcactg attatgaatc cctctgatcc 349

tactctctga agacctcttg ggggtccaaca tccaaataaa gcgacatccc aaaaaaaaaa 409

aaaaaaaaaa 419

<210> 315  
<211> 81  
<212> PRT  
<213> Conus tessulatus

<400> 315

Met Lys Leu Thr Cys Val Val Val Val Ala Val Leu Phe Leu Asn Ala  
1 5 10 15

Trp Thr Phe Ala Thr Ala Val Asp Ser Lys His Ala Leu Ala Lys Leu  
20 25 30

Phe Met Lys Ala Arg Asp Glu Met Tyr Asn Pro Asp Ala Thr Lys Leu  
35 40 45

0949637-122800

ctg ttt gaa gca caa tgc tgc gat ggc tgg tgc ttt ttc gtc tgc atg 240  
Leu Phe Glu Ala Gln Cys Cys Asp Gly Trp Cys Phe Phe Val Cys Met  
65 70 75

<220>  
<221> CDS  
<222> (7) .. (234)

```

<400>      320
ggatcc atg aaa ctg acg tgt gtg gtg atc gtt gct gtg ctg ttc ttg      48
      Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
      1          5          10

acc gcc tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag      96
Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu
15          20          25          30

aat ctt ttt ccg aag gca cgt cac gaa atg aag aac ccc gaa gcc tct      144
Asn Leu Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser
      35          40          45

aaa ttg aac aag agg tgc gtt gac cct ggt gaa ttt tgt ggt ccg gga      192
Lys Leu Asn Lys Arg Cys Val Asp Pro Gly Glu Phe Cys Gly Pro Gly
      50          55          60

ttt gga gat tgc tgc act ggc ttc tgc ctt tta gtc tgc atc      234
Phe Gly Asp Cys Cys Thr Gly Phe Cys Leu Leu Val Cys Ile
      65          70          75

taaaactgcc gtgatgtctt ctactcccat ctgtgctacc cctcgag      281

<210>      321
<211>      76
<212>      PRT
<213>      Conus characteristicus

<400>      321

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1          5          10          15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
      20          25          30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
      35          40          45

Asn Lys Arg Cys Val Asp Pro Gly Glu Phe Cys Gly Pro Gly Phe Gly
      50          55          60

Asp Cys Cys Thr Gly Phe Cys Leu Leu Val Cys Ile
65          70          75

<210>      322
<211>      25
<212>      PRT
<213>      Conus characteristicus

<220>
<221>      SITE
<222>      (1)..(25)
<223>      Xaa at residues 4 and 10 may be Pro or hydroxy-Pro; Xaa at residu
e 6 may be Glu or gamma-carboxy-Glu

<400>      322

```



Cys Val Asp Xaa Gly Xaa Phe Cys Gly Xaa Gly Phe Gly Asp Cys Cys  
1 5 10 15

Thr Gly Phe Cys Leu Leu Val Cys Ile  
20 25

<210> 323  
<211> 287  
<212> DNA  
<213> Conus miliaris

<220>  
<221> CDS  
<222> (7)..(240)

<400> 323  
ggatcc atg aaa ctg acg tgc gtg gtg atc gtt gct gtg ttg ttc ttg 48  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu  
1 5 10

acc gcc tgg aca ttc gtc atg gct gat gac tcc aga aat gat ttg gag 96  
Thr Ala Trp Thr Phe Val Met Ala Asp Asp Ser Arg Asn Asp Leu Glu  
15 20 25 30

aat ctt ttt ctg aag gca cgt cat gaa atg aag aac ccc gaa gct tct 144  
Asn Leu Phe Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser  
35 40 45

aaa ttg aac aag aga tgc ctt cca aat ggt gta ctt tgt gat ctg gga 192  
Lys Leu Asn Lys Arg Cys Leu Pro Asn Gly Val Leu Cys Asp Leu Gly  
50 55 60

tct cca cca tac tgc tgc agt ggc tgg tgc gcg atc gtc gtc tgc atc 240  
Ser Pro Pro Tyr Cys Cys Ser Gly Trp Cys Ala Ile Val Val Cys Ile  
65 70 75

taaaactgtc gtcattgtctt ctactcccat ctgtgctacc cctcgag 287

<210> 324  
<211> 78  
<212> PRT  
<213> Conus miliaris

<400> 324

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Met Ala Asp Asp Ser Arg Asn Asp Leu Glu Asn Leu  
20 25 30

Phe Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

Asn Lys Arg Cys Leu Pro Asn Gly Val Leu Cys Asp Leu Gly Ser Pro  
50 55 60

Pro Tyr Cys Cys Ser Gly Trp Cys Ala Ile Val Val Cys Ile

003333" 4964260

75

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<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residues 3, 13 and 14 may be Pro or hydroxy-Pro; Xaa at residue 15 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 20 may be Trp or bromo-Trp
```

Cys Ser Gly Xaa Cys Ala Ile Val Val Cys Ile  
20 25

```
<220>
<221> CDS
<222> (7)..(240)
```

taaaactgcc gtgatgtggt ctactcccat ctgtgctacc cctcgag 287

<400> 327

aat ctt ttt tgc aag gca cat cac gaa atg aag aac ccc gaa gcc tct 144  
Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser  
35 40 45

gaa caa aac tgc tgc tat acc tat tgc ttt att gta gtc tgc cta 237  
Glu Gln Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu  
65 70 75

```
<210> 330
<211> 77
<212> PRT
<213> Conus lividus
```

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu  
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln  
50 55 60

Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu  
65 70 75

```
<210> 331
<211> 26
<212> PRT
<213> Conus lividus
```

```
<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residue 2 may be Pro or hydroxy-Pro; Xaa at residues 6 and
      12 may be Glu or gamma-carboxy-Glu; Xaa at residues 17 and 19 ma
      y be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
      O-phospho-Tyr
```

Cys Xaa Asn Thr Gly Xaa Leu Cys Asp Val Val Xaa Gln Asn Cys Cys  
1 5 10 15

Xaa Thr Xaa Cys Phe Ile Val Val Cys Leu  
20 25

<210>	332
<211>	281
<212>	DNA

<221> SITE

<222> (1)..(25)

<223> Xaa at residues 3, 13 and 14 may be Glu or gamma-carboxy-Glu; Xaa at residue 10 may be Pro or hydroxy-Pro; Xaa at residues 12 and 22 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 334

Cys Val Xaa Asp Gly Asp Phe Cys Gly Xaa Gly Xaa Xaa Xaa Cys Cys  
1 5 10 15

Ser Gly Phe Cys Leu Xaa Val Cys Ile  
20 25

<210> 335

<211> 293

<212> DNA

<213> *Conus generalis*

<220>

<221> CDS

<222> (7)..(249)

<400> 335

ggatcc atg aaa ctg acg tgt gtg gtg atc gtt gct gtg cta ttc ttg 48  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu  
1 5 10

acc gcc tgg aca ttc gtc acg gct gat gac acc aga tat aaa ctg gag 96  
Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Thr Arg Tyr Lys Leu Glu  
15 20 25 30

aat cct ttt ctg aag gca cgc aac gaa ctg cag aaa cac gaa gcc tct 144  
Asn Pro Phe Leu Lys Ala Arg Asn Glu Leu Gln Lys His Glu Ala Ser  
35 40 45

caa ctg aac gag aga ggc tgc ctt gac cca ggt tac ttc tgt ggg acg 192  
Gln Leu Asn Glu Arg Gly Cys Leu Asp Pro Gly Tyr Phe Cys Gly Thr  
50 55 60

cgc ttt ctt gga gca tac tgc tgc ggt ggc att tgc ctt att gtc tgc 240  
Pro Phe Leu Gly Ala Tyr Cys Cys Gly Gly Ile Cys Leu Ile Val Cys  
65 70 75

ata gaa acg taaaggcttg atgtcttcta ctcccatctg tgctaccct ctag 293  
Ile Glu Thr  
80

<210> 336

<211> 81

<212> PRT

<213> *Conus generalis*

<400> 336

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Thr Arg Tyr Lys Leu Glu Asn Pro  
20 25 30

003221" / E964/60

Phe Leu Lys Ala Arg Asn Glu Leu Gln Lys His Glu Ala Ser Gln Leu  
 35 40 45

Asn Glu Arg Gly Cys Leu Asp Pro Gly Tyr Phe Cys Gly Thr Pro Phe  
 50 55 60

Leu Gly Ala Tyr Cys Cys Gly Gly Ile Cys Leu Ile Val Cys Ile Glu  
 65 70 75 80

Thr

<210> 337  
 <211> 30  
 <212> PRT  
 <213> Conus generalis

<220>  
 <221> SITE  
 <222> (1)..(30)  
 <223> Xaa at residues 5 and 12 may be Pro or hydroxy-Pro; Xaa at residues 7 and 17 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 337

Gly Cys Leu Asp Xaa Gly Xaa Phe Cys Gly Thr Xaa Phe Leu Gly Ala  
 1 5 10 15

Xaa Cys Cys Gly Gly Ile Cys Leu Ile Val Cys Ile Xaa Thr  
 20 25 30

<210> 338  
 <211> 400  
 <212> DNA  
 <213> Conus episcopatus

<220>  
 <221> CDS  
 <222> (7)..(234)

<400> 338  
 ggatcc atg aaa ctg acg tgc gtg gtg atc gtt gct gtg ctg ttc ttg 48  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu  
 1 5 10

acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg 96  
 Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly  
 15 20 25 30

aat ctt ttt tcg aat gta cat cac gaa atg aag aac ctc gaa gac tct 144  
 Asn Leu Phe Ser Asn Val His His Glu Met Lys Asn Leu Glu Asp Ser  
 35 40 45

aaa ttg gac aag aag tgc ctt ggg ttt ggt gaa gct tgt ctt atg ctt 192  
 Lys Leu Asp Lys Lys Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu  
 50 55 60

008222T " 2964250





&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (7)..(240)

&lt;400&gt; 341

ggatcc atg aaa ctg acg tgc gtg gtg atc att gct gtg ctg ttc ttg 48  
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu  
 1 5 10

acc gcc tgg aca ttc gtc atg gct gat gac ccc aga gat gaa ccg gag 96  
 Thr Ala Trp Thr Phe Val Met Ala Asp Asp Pro Arg Asp Glu Pro Glu  
 15 20 25 30

gca cgt gac gaa atg aac ccc gca gcc tct aaa ttg aac gag aga ggc 144  
 Ala Arg Asp Glu Met Asn Pro Ala Ala Ser Lys Leu Asn Glu Arg Gly  
 35 40 45

tgc ctt gca gtt gat tat ttt tgc ggc ata ccg ttt gtg agc aac ggc 192  
 Cys Leu Ala Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Ser Asn Gly  
 50 55 60

cta tgc tgc agt ggc aat tgt gtt ttt gtc tgc aca ccc caa ggg aag 240  
 Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Pro Gln Gly Lys  
 65 70 75

taaaactgcc gtgacgtctt ctactcccct ctgtgctacc tggcttgatc tttgattggc 300

gtgtgcactt cactgggttat gaacccctct gatcctactc totgaagacc tctgggggtcc 360

aacatccaaa taaagcgaca tcccacaaaa aaaaaaaaaa aaaa 404

&lt;210&gt; 342

&lt;211&gt; 78

&lt;212&gt; PRT

&lt;213&gt; Conus episcopatus

&lt;400&gt; 342

Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Val Met Ala Asp Asp Pro Arg Asp Glu Pro Glu Ala Arg  
 20 25 30

Asp Glu Met Asn Pro Ala Ala Ser Lys Leu Asn Glu Arg Gly Cys Leu  
 35 40 45

Ala Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Ser Asn Gly Leu Cys  
 50 55 60

Cys Ser Gly Asn Cys Val Phe Val Cys Thr Pro Gln Gly Lys  
 65 70 75

&lt;210&gt; 343

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Conus episcopatus

009493 "12900

<220>  
 <221> SITE  
 <222> (1)..(31)  
 <223> Xaa at residue 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 12 and 30 may be Pro or hydroxy-Pro

<400> 343

Gly Cys Leu Ala Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Ser Asn  
 1 5 10 15

Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Xaa Gln  
 20 25 30

<210> 344  
 <211> 202  
 <212> DNA  
 <213> Conus achatinus

<220>  
 <221> CDS  
 <222> (85)..(171)

<400> 344

cgatcctctg tcctccatct attattatttc gctgccaaac tgtgttaaatt attcaagtct 60

ctctttctgt ttgtgtctaa cagg ttg aga tgg tgc att cct aga ggt gat 111  
 Leu Arg Trp Cys Ile Pro Arg Gly Asp  
 1 5

ctt tgt ttc ccc tcg gat cgc ata caa tgc tgc agt ggc aag tgc aca 159  
 Leu Cys Phe Pro Ser Asp Arg Ile Gln Cys Cys Ser Gly Lys Cys Thr  
 10 15 20 25

ttc gtc tgc atg taaaactgcc gtgatgtctt ctctccct c 202  
 Phe Val Cys Met

<210> 345  
 <211> 29  
 <212> PRT  
 <213> Conus achatinus

<400> 345

Leu Arg Trp Cys Ile Pro Arg Gly Asp Leu Cys Phe Pro Ser Asp Arg  
 1 5 10 15

Ile Gln Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met  
 20 25

<210> 346  
 <211> 27  
 <212> PRT  
 <213> Conus achatinus

<220>  
 <221> SITE  
 <222> (1)..(27)

008227" 4E964460

<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 11 may be Pro or hydroxy-Pro

<400> 346

Xaa Cys Ile Xaa Arg Gly Asp Leu Cys Phe Xaa Ser Asp Arg Ile Gln  
1 5 10 15

Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met  
20 25

<210> 347

<211> 202

<212> DNA

<213> Conus achatinus

<220>

<221> CDS

<222> (85)..(171)

<400> 347

cgatcctctg tctcctcctc tcattcattc gctgccaaac tgtattaaat attcgaatct 60

ctctttctgt ttgtgtctga caga ttg aga ggg tgc gtt cct agt ggt gaa 111  
Leu Arg Gly Cys Val Pro Ser Gly Glu  
1 5

att tgt tac ttc atg gat cac ata gga tgc tgc agt ggc aag tgc aca 159  
Ile Cys Tyr Phe Met Asp His Ile Gly Cys Cys Ser Gly Lys Cys Thr  
10 15 20 25

ttc gtc tgc atg taaaactgcc gtgatgtctt ctctcccat c 202  
Phe Val Cys Met

<210> 348

<211> 29

<212> PRT

<213> Conus achatinus

<400> 348

Leu Arg Gly Cys Val Pro Ser Gly Glu Ile Cys Tyr Phe Met Asp His  
1 5 10 15

Ile Gly Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met  
20 25

<210> 349

<211> 27

<212> PRT

<213> Conus achatinus

<220>

<221> SITE

<222> (1)..(27)

<223> Xaa at residue 4 may be Pro or hydroxy-Pro; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 10 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

00822T 1260

Asn Lys Lys Asp Glu Cys Ser Ala Pro Gly Ala Phe Cys Leu Ile Arg  
50 55 60

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<210> 354
<211> 82
<212> PRT
<213> Conus bullatus
```

96

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<210> 357
<211> 79
<212> PRT
<213> Conus striolatus
```

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Pro Gln Thr Thr Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

Asn Gln Thr Asp Cys Leu Ala Lys Asp Ala Phe Cys Ala Trp Pro Ile  
50 55 60

Leu Gly Pro Leu Cys Cys Ser Arg Leu Cys Leu Tyr Val Cys Met  
65 70 75

```
<210> 358
<211> 28
<212> PRT
<213> Conus striolatus
```

```

<220>
<221> SITE
<222> (1)..(28)
<223> Xaa at residue 11 may be Trp or bromo-Trp; Xaa at residues 12 and
      16 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Tyr, 125-
      I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr.

```

Asp Cys Leu Ala Lys Asp Ala Phe Cys Ala Xaa Xaa Ile Leu Gly Xaa  
1 5 10 15

Leu Cys Cys Ser Arg Leu Cys Leu Xaa Val Cys Met  
20 25

1151 P. 807-15





```

<400> 365
cgatccatct gtccatccat ctattcattc attcgctgcc aaactgtatt aaatatccaa      60

gtctctcttt ctgtttgtgt ct aac aga ttg a,t agg tgc att cct agt ggt      112
      Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
      1             5             10

```

gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctactcccct c 206



<400> 372

Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu  
20 25 30

```

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residues 3 and 10 may be Pro or hydroxy-Pro.

```

<400> 373

Cys Ser Ala Lys Cys Ala Phe Val Cys Leu  
20 25

```
<220>
<221> CDS
<222> (83)..(175)
```

```

<400> 374
cgatccatct gtccatccat ctattcattc attcgtgcc aaactgtatt aaatattcaa      60

gtctctcttt ctgttttgtgt ct aac aga ttg agt agg tgc att cct agt ggt      112
                        Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
                        1          5          10

gat ctt tgt ttc ccc tcg gat cac ata caa tgc tgc aat gcc gag tgc      160
Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Glu Cys
                        15          20          25

gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctctctccct c      206
Ala Phe Val Cys Leu
                        30

```

```
<210> 375
<211> 31
<212> PRT
<213> Conus circumcissus
```

&lt;400&gt; 375

Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser  
 1 5 10 15

Asp His Ile Gln Cys Cys Asn Ala Glu Cys Ala Phe Val Cys Leu  
 20 25 30

&lt;210&gt; 376

&lt;211&gt; 26

&lt;212&gt; PRT

&lt;213&gt; Conus circumciscus

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (1)..(26)

&lt;223&gt; Xaa at residues 3 and 10 may be Pro or hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu

&lt;400&gt; 376

Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys  
 1 5 10 15

Cys Asn Ala Xaa Cys Ala Phe Val Cys Leu  
 20 25

&lt;210&gt; 377

&lt;211&gt; 206

&lt;212&gt; DNA

&lt;213&gt; Conus circumciscus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (83)..(175)

&lt;400&gt; 377

cgatccatct gtccatccat ctattcattc attcgtgtgc aaactgtatt aaatattcaa 60

gtctctcttt ctgttttgtt ct aac aga ttg agt tgg tgc att cct agt ggt 112  
 Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly  
 1 5 10

gat ctt tgt ttc ccc tcg gat cac ata cga tgc tgc agt gcc aag tgc 160  
 Asp Leu Cys Phe Pro Ser Asp His Ile Arg Cys Cys Ser Ala Lys Cys  
 15 20 25

gca ttc gtc tgc ttg taaaactgcc gtgatgtott ctottcccat c 206  
 Ala Phe Val Cys Leu  
 30

&lt;210&gt; 378

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Conus circumciscus

&lt;400&gt; 378

Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser  
 1 5 10 15

Asp His Ile Gln Cys Cys Asn Ala Lys Cys Ala Phe Ala Cys Leu  
20 25 30

<210>	385
<211>	27
<212>	PRT



$\langle 220 \rangle$ 

<222> (1) .. (27)

<400> 385

Cys Cys Asn Ala Lys Cys Ala Phe Val Cys Leu  
20 25

<211> 200

<212> DNA

 $\langle 220 \rangle$ 

<221> CDS

<400> 386

ctttctgttt gtgtct aac aga ttg agt tgg tgc att cct act ggt gat ctt 112  
Asn Arg Leu Ser Trp Cys Ile Pro Thr Gly Asp Leu  
1 5 10

tgt ttc ccc tgg gat cac ata caa tgc tgc agt ggc aag tgc aca ttc 160  
Cys Phe Pro Ser Asp His Ile Gln Cys Cys Ser Gly Lys Cys Thr Phe  
15 20 25

gtc tgc atg taaaactgcc gtgatgtctt ctctctccct c 200  
Val Cys Met  
30

<210> 387

<211> 31

<212> PRT

<400> 387

Asn Arg Leu Ser Trp Cys Ile Pro Thr Gly Asp Leu Cys Phe Pro Ser  
1 5 10 15

Asp His Ile Gln Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met  
20 25 30

<210> 388

<211> 27

<212> PRT

 $\langle 220 \rangle$ 

<221> SITE

<222> (1)..(27)

<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 11 may be Pro or hydroxy-Pro

<400> 388

Xaa Cys Ile Xaa Thr Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln  
1 5 10 15

Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met  
20 25

<210> 389

<211> 266

<212> DNA

<213> Conus monachus

<220>

<221> CDS

<222> (1)..(246)

<400> 389

atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctt 96  
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu  
20 25 30

tct ccg aag gca cgt cac gaa atg aag aac ccc gaa gcc tct aaa tcg 144  
Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser  
35 40 45

aac aag aga tat gag tgc tat tct act ggt aca ttt tgt ggc atc aac 192  
Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn  
50 55 60

gga gga ctc tgc tgc agc aac ctt tgc tta ttt ttc gtg tgc tta aca 240  
Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr  
65 70 75 80

ttt tcg tgatgtcttc tcctccctc 266  
Phe Ser

<210> 390

<211> 82

<212> PRT

<213> Conus monachus

<400> 390

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu  
20 25 30

Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser

35

40

45

Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn  
 50 55 60

Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr  
 65 70 75 80

Phe Ser

<210> 391

<211> 31

<212> PRT

<213> Conus monachus

<220>

<221> SITE

<222> (1)..(31)

<223> Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be Glu or gamma-carboxy-Glu

<400> 391

Xaa Xaa Cys Xaa Ser Thr Gly Thr Phe Cys Gly Ile Asn Gly Gly Leu  
 1 5 10 15

Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser  
 20 25 30

<210> 392

<211> 277

<212> DNA

<213> Conus stercusmuscarum

<220>

<221> CDS

<222> (1)..(246)

<400> 392

atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

tgg aca ttc gtc aca gct gat gac tcc ata aat gga ccg gag aat aga 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Pro Glu Asn Arg  
 20 25 30

cga ata tgg gag aaa ctt ttg ttg aag gca cgt gac gaa atg aag aac 144  
 Arg Ile Trp Glu Lys Leu Leu Leu Lys Ala Arg Asp Glu Met Lys Asn  
 35 40 45

ccc gaa gcc tct caa ttg aga tgg tgc att cct agt ggt gaa ctt tgt 192  
 Pro Glu Ala Ser Gln Leu Arg Trp Cys Ile Pro Ser Gly Glu Leu Cys  
 50 55 60

ttc cgc tcg gat cac ata caa tgc tgc agt gcc aag tgc gca ttc gtc 240  
 Phe Arg Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val

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<210> 395
<211> 266
<212> DNA
<213> Conus stercusmuscarum
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<400> 395

tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg aag aat ctt 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu  
 20 25 30

aac aag aga gat ggg tgc tct agt ggt ggt aca ttt tgt ggc atc cgt 192  
Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg  
50 55 60

att gat tgatgtcttc tattcccttc 266  
Ile Asp

<400> 396

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu  
20 25 30

Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg  
50 55 60

Ile Asp

<210>	397
<211>	31
<212>	PRT

$\langle 220 \rangle$ 

<222> (1) .. (31)

<223> Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 25 may be Trp or bromo-Trp

Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg Xaa Gly Leu  
1 5 10 15

Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Ile Asp  
20 25 30

<210> 398

<211> 265

<212> DNA

<213> Conus striolatus

 $\langle 220 \rangle$ 

<221> CDS

 $\langle 222 \rangle \quad (1) \dots (234)$ 

<400> 398

atg aaa ctg acg tgc ata atg acc gtt gct gtg ctg ttc ttg acc gct 48  
Met Lys Leu Thr Cys Ile Met Thr Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctt      96  
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu  
                20                         25                         30

ctt ctg aag aca cgt cac gaa gtg gaa aac ccc aaa gcc tct agg tcg 144  
Leu Leu Lys Thr Arg His Glu Val Glu Asn Pro Lys Ala Ser Arg Ser  
35 40 45

ggc ggt agg tgc cgt cct ggt ggt acg gtt tgt ggc ttt ccg aaa cct 192  
Gly Gly Arg Cys Arg Pro Gly Gly Thr Val Cys Gly Phe Pro Lys Pro  
50 55 60

gga cca tac tgc tgc agt ggc tgg tgc ttt ttt gtc tgc gcc 234  
Gly Pro Tyr Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Ala  
65 70 75

taaacctgcc gtgatgtctt ctctcccat c 265

<210> 399

<211> 78

<212> PRT

<213> Conus striolatus

<400> 399

Met Lys Leu Thr Cys Ile Met Thr Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu  
20 25 30

Leu Leu Lys Thr Arg His Glu Val Glu Asn Pro Lys Ala Ser Arg Ser  
 35 40 45

Gly Gly Arg Cys Arg Pro Gly Gly Thr Val Cys Gly Phe Pro Lys Pro  
 50 55 60

Gly Pro Tyr Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Ala  
 65 70 75

<210> 400  
 <211> 27  
 <212> PRT  
 <213> Conus striolatus

<220>  
 <221> SITE  
 <222> (1)..(27)  
 <223> Xaa at residues 3, 11, 13 and 15 may be Pro or hydroxy-Pro; Xaa at residue 16 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 21 may be Trp or bromo-Trp

<400> 400

Cys Arg Xaa Gly Gly Thr Val Cys Gly Phe Xaa Lys Xaa Gly Xaa Xaa  
 1 5 10 15

Cys Cys Ser Gly Xaa Cys Phe Phe Val Cys Ala  
 20 25

<210> 401  
 <211> 272  
 <212> DNA  
 <213> Conus striolatus

<220>  
 <221> CDS  
 <222> (1)..(243)

<400> 401

atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg act gcc 48  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aaa aat gga ctg gag aat cat 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His  
 20 25 30

ttt tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg 144  
 Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu  
 35 40 45

gac aaa aag gaa gcc tgc tat ccg cct ggt act ttt tgt ggc ata aag 192  
 Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys  
 50 55 60

ccc ggg cta tgc tgc agt gag ttg tgt tta ccg gcc gtc tgc gtc ggt 240  
 Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly

008221" 15967460

65

70

75

80

ggt taactgccgt gatgtcttct attcccctc  
Gly

272

&lt;210&gt; 402

&lt;211&gt; 81

&lt;212&gt; PRT

&lt;213&gt; Conus striolatus

&lt;400&gt; 402

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His  
20 25 30

Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu  
35 40 45

Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys  
50 55 60

Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly  
65 70 75 80

Gly

&lt;210&gt; 403

&lt;211&gt; 29

&lt;212&gt; PRT

&lt;213&gt; Conus striolatus

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (1)..(29)

<223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at  
residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-s  
ulpho-Tyr or O-phospho-Tyr; Xaa at residues 5, 6, 14 and 24 may b  
e Pro or hydroxy-Pro

&lt;400&gt; 403

Xaa Ala Cys Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu  
1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Xaa Ala Val Cys Val Gly  
20 25

&lt;210&gt; 404

&lt;211&gt; 265

&lt;212&gt; DNA

&lt;213&gt; Conus striolatus

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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(246)

&lt;400&gt; 404

atg	aaa	ctg	acg	tgt	ctg	atg	gct	gtt	gct	gtg	ctg	ttc	ttg	acc	gcc	48
Met	Lys	Leu	Thr	Cys	Leu	Met	Ala	Val	Ala	Val	Leu	Phe	Leu	Thr	Ala	
1				5				10					15			

cgg	aca	ttc	gtc	acg	gct	gat	gac	tcc	aga	aat	gga	ttg	gag	aat	ctt	96
Arg	Thr	Phe	Val	Thr	Ala	Asp	Asp	Ser	Arg	Asn	Gly	Leu	Glu	Asn	Leu	
			20					25					30			

tct	ccg	aag	gca	cgt	cac	gaa	atg	aag	aac	ccc	gaa	gcc	tct	aaa	tcg	144
Ser	Pro	Lys	Ala	Arg	His	Glu	Met	Lys	Asn	Pro	Glu	Ala	Ser	Lys	Ser	
		35					40					45				

aac	aag	aga	tat	gag	tgc	tat	tct	act	ggt	aca	ttt	tgt	ggc	atc	aac	192
Asn	Lys	Arg	Tyr	Glu	Cys	Tyr	Ser	Thr	Gly	Thr	Phe	Cys	Gly	Ile	Asn	
	50					55					60					

gga	gga	ctc	tgc	tgc	agc	aac	ctt	tgc	tta	ttt	ttc	gtg	tgc	tta	aca	240
Gly	Gly	Leu	Cys	Cys	Ser	Asn	Leu	Cys	Leu	Phe	Phe	Val	Cys	Leu	Thr	
65					70					75				80		

ttt	tcg	tgatgtcttc	tatccccctc													265
Phe	Ser															

&lt;210&gt; 405

&lt;211&gt; 82

&lt;212&gt; PRT

&lt;213&gt; Conus striolatus

&lt;400&gt; 405

Met	Lys	Leu	Thr	Cys	Leu	Met	Ala	Val	Ala	Val	Leu	Phe	Leu	Thr	Ala
1				5				10						15	

Arg	Thr	Phe	Val	Thr	Ala	Asp	Asp	Ser	Arg	Asn	Gly	Leu	Glu	Asn	Leu
			20					25					30		

Ser	Pro	Lys	Ala	Arg	His	Glu	Met	Lys	Asn	Pro	Glu	Ala	Ser	Lys	Ser
		35					40					45			

Asn	Lys	Arg	Tyr	Glu	Cys	Tyr	Ser	Thr	Gly	Thr	Phe	Cys	Gly	Ile	Asn
	50					55					60				

Gly	Gly	Leu	Cys	Cys	Ser	Asn	Leu	Cys	Leu	Phe	Phe	Val	Cys	Leu	Thr
65					70					75				80	

Phe Ser

&lt;210&gt; 406

&lt;211&gt; 31

Cys His Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg

20

25

30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys  
 35 40 45

Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg Ile Cys Cys Gly Tyr Cys  
 50 55 60

Ala Tyr Phe Gly Lys Ile Cys Ile Gly Tyr Pro Lys Asn  
 65 70 75

<210> 409

<211> 35

<212> PRT

<213> Conus striolatus

<220>

<221> SITE

<222> (1)..(35)

<223> Xaa at residues 10, 21, 24 and 32 may be Tyr, 125-I-Tyr, mono-iod  
 o-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue  
 33 may be Pro or hydroxy-Pro

<400> 409

Ser Thr Ser Cys Met Lys Ala Gly Ser Xaa Cys Val Ala Thr Thr Arg  
 1 5 10 15

Ile Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Ile Cys Ile Gly Xaa  
 20 25 30

Xaa Lys Asn  
 35

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